Spring 5-2011

Analysis of Long-term Selection (28 generations) for Reproduction, Growth, and Carcass Traits in Swine

Wan-Ling Hsu
University of Nebraska-Lincoln, birdyalaska@gmail.com

Analysis of Long-term Selection (28 generations) for Reproduction, Growth, and Carcass Traits in Swine

by

Wan-Ling Hsu

A Dissertation

Presented to the Faculty of

The Graduate College at the University of Nebraska

In Partial Fulfillment of Requirements

For the Degree of Doctor of Philosophy

Major: Animal Science

Under the Supervision of Professor Rodger K. Johnson

Lincoln, Nebraska

May, 2011

Analysis of Long-term Selection (28 generations) for Reproduction, Growth, and Carcass Traits in Swine

Wan-Ling Hsu, Ph.D.
University of Nebraska, 2011

Advisor: Rodger K. Johnson

The objectives were 1) to estimate responses from 28 generations of selection for increased pigs born alive (BA) with additional selection for increased 180 d weight (WT) and longissimus muscle area (LMA) and decreased backfat (BF) in the last eight generations, 2) to estimate genetic parameters for an array of traits, and 3) to investigate whether a plateau in response for BA has occurred. All lines were derived from the same Large White/Landrace composite population. Index selection for ovulation rate and embryo survival (G0-11) was initiated in L2 in 1981; L1 was selected randomly control line for L2 (G0-23). L2 was subsequently selection for fully formed pigs or BA during G12-28, and WT, BF and LMA (G20-28). At G8, L4 was derived from L2; L5 and L6 were derived from L1. L4 and L5 were in two-stage selection for ovulation rate and litter size (G9-16) and for BA (G17-19); L6 was selected randomly. L4 and L5 were crossed in G20 to form L45 which was selected for BA, WT, LMA and BF thereafter. Line sizes each generation were 40-60 litters by 15-20 sires. MTDFREML was used to obtain estimates of variance components, EBVs and responses for 17 traits (n = 1,883 ~ 54,174). Responses and cumulative selection differentials (CSD) were estimated by linear and quadratic regression of

mean EBVs and phenotypes on generation for each line. Genetic trend and CSDs for BA were linear or quadratic in all selection lines ($P < 0.05$). Direct and indirect selection on BA was effective. Genetic correlations of reproduction with growth and carcass traits were small. BA, WT, and LMA increased and BF decreased in all selection lines ($P < 0.05$). For BA, genetic variance in selection lines during G20-28 still exhibit, and changes in CSDs and mean EBVs were linear ($P < 0.01$), but not quadratic. There was no evidence for a plateau in BA after 28 generations of selection.

Key Words: carcass, growth, long-term selection, reproduction, swine

Acknowledgements

First of all, I would like to thank my advisor, Dr. Rodger K. Johnson, for allowing me the opportunity to be his student and to thank him for postponing his retirement date for me. I thank him for sharing his knowledge and experience. I deeply appreciate his patience, encouragement, advice and guidance. I really enjoyed learning and working with him. I am proud to be his last PhD student.

I would also like to thank Dr. Merlyn K. Nielsen, Dr. Phillip S. Miller and Dr. P. Stephen Baenziger for serving on my committee and for making me think. I appreciate their patience and comments on my research. I thank Dr. Nielsen for sharing his knowledge and experience about science and personality. I thank Dr. Miller for improving my knowledge of another field and for giving me advice and for making me think among connection among nutrition, genetics and physiology. I thank Dr. Baenziger for his thoughtful suggestions and for sharing his philosophy of life by applying the method of selection index. Thanks again to my advisor and my committee for making me feel comfortable while learning from them.

I must thank my M.S. advisor, Dr. L. Dale Van Vleck. He is like a grandfather and best friend to me. His door was always open to share his wisdom, experience, jokes and snacks with me, even though he was already retired. I deeply appreciate his

kindness, encouragement and patience over my graduate life. I enjoy being part of his family.

I would also like to thank Dr. Jess Miner, Dr. Daniel Ciobanu, Dr. Brett White and other faculty members in Department of Animal Science, and Dr. Sy-Hwang Liou in Department of Physics and Astronomy at UNL, and Dr. En-Chung Lin in Department Animal Science and Technology at National Taiwan University for their advice and support. Thanks to friendly Mrs. Sherri Pitchie for her assistance with many things.

Thanks to Huyen, Pamela, Lasika, Amy, Qiao, Boan, Shuo, Chao-Mei, Xiang, Alberto, Sungwon, Chanho, Autumn, Tim and the other graduate students for support and for discussions with me about my project. Thanks to Penny, Elaine, Abby, Fion, Yu-Chin, Ya-Ting, Ping, Mia, Claire, Jenny, Esther, Keziah, Sherry, Angela, Mandy, Ivan, Kevin and the other friends for support and helping me enjoy my graduate life.

Thanks to Dr. Sy-Hwang Liou and aunt Mei-Lan Lin; Dr. Steven Wang and Dr. Nancy Wang; Dr. Tsang-Yi Lin and aunt Susan Huang; Dr. Chuan-Yu Wang and aunt Mei-Huey Su; Dr. Pau Lu and aunt Janet Lu; uncle Paul Yang and aunt Annie Yang; sister Coral Su and her husband Taka; aunt Tsai-Ching and the other Taiwanese families in Lincoln for treating me like a family member.

A special thank you goes to the Department of Animal Science for funding to support my program.

Finally, I would like to thank my funny family for their support and encouragement. Especially, I would like to express my appreciation for love, jokes and financial support from my dad and mom, Ching-Rung Hsu and Jin-Luan Liou, and for constant encouragement and support from my grandparents, Chu-Sha Hsu, Weng Luen Hsu, Ching-Jung Liou and Chuen-Tsau Chen Liou; my sister, Yu-Ling; and my brothers, Hung-Jin and Hung-Shang. I would also like to thank my American family, Fred, Phyllis, Mike, Deb, Amy, Matt, Erin and Ethan, for their encouragement and for sharing of important things in life.

My program would have never been accomplished without those important persons and the Department of Animal Science. Again, thank you all for making my life so colorful, wonderful and meaningful.

Table of Contents

List of Tables

Materials and Methods:

Results and Discussion:

List of Figures

Materials and Methods:

Results and Discussion:

Chapter 1

General Introduction

Increasing producing ability of livestock is always a goal for breeders in the commercial livestock industry. Reproductive, growth and carcass traits are important economic traits for swine breeders. Fredeen and Mikami (1986a, 1986b, 1986d) showed that direct selection for growth rate and backfat depth is effective. In recent years, industry selection has increased growth rate (low to moderate heritability) and decreased backfat depth (high heritability). Schinckel et al. (1998) concluded that economic value of reproductive traits has become more and more important relative to growth and backfat depth. However, among quantitative traits of swine, reproductive traits are the hardest to improve by selection because heritabilities of most reproductive traits are low.

Litter size is the most common measure of a sow's reproductive performance (Tess et al., 1983; Holl and Robison, 2003). Direct selection for increased litter size has been successful using hyper-prolific breeding schemes in a large population with very high selection intensity (Sorensen et al., 2000; Noguera et al., 2002). Tribout et al. (2003) obtained an increase of three French Large White piglets after 15 years of selection. However, direct selection for litter size may not be very practical in smaller populations (Pérea-Enciso and Bidanel, 1997), but direct selection for litter size after

selection for ovulation rate was effective (Lamberson et al., 1991; Johnson et al., 1999). Direct selection for increased litter size in smaller populations has not resulted in significant response (Ollivier, 1982; Haley et al., 1988; Bolet et al., 1989) or has resulted in little response (Estany et al., 2002; Holl and Robison, 2003) in swine and in mice (Bakker et al., 1878). However, the study reported here will show that direct selection for increased fully formed pigs or increased born alive pigs in a small, closed population is effective.

Many alternatives to direct selection for litter size have been proposed. These include index selection for components (ovulation rate and embryonic survival) of litter size (Johnson et al., 1984; Neal et al., 1989; Bennett and Leymaster, 1989, 1990a, 1990b; Johnson et al., 1999; Ruiz-Flores and Johnson, 2001; Rosendo et al., 2007a), selection for uterine capacity (Bennett and Leymaster, 1990a; Blasco et al., 2005; Santacreu et al., 2005), selection for prenatal survival (Bradford, 1979; Rosendo et al., 2007b), selection for placental traits (Wilson et al., 1999 and Mesa et al., 2005), selection for ovulation rate. Implementation of these methods resulted in increased mean litter size in small populations of swine, rabbits and mice. The current study will show that index selection for ovulation rate and embryo survival and two-stage selection for increased ovulation rate and litter size increased fully formed pigs and live pigs per litter.

From estimates of heritabilities and genetic correlations, Johnson et al. (1984)

calculated an index of ovulation rate and embryo survival that caused greater expected response in litter size than direct selection. Part of the increase occurred because of greater expected response in litter size at the same selection intensity. Additional expected response occurred by implementation of a protocol in which all females each generation are mated and traits recorded via laparotomy at 50 d of gestation, which resulted in traits being recorded in a larger number of females and greater selection intensity. Based on simulation of expected responses from selection for ovulation rate, uterine capacity, and potential embryonic survival (Bennett and Leymaster, 1989, 1990a), Bennett and Leymaster (1990b) suggested selection for an index of ovulation rate and uterine capacity, an index of ovulation rate and embryo survival or an index of ovulation rate and litter size would increase litter size more than direct selection for litter size. Johnson et al. (1999) reported results of 11 generations of selection for an index of ovulation rate and embryonic survival to 50 d of gestation followed by 3 generations of direct selection for litter size. An increase of 2.3 piglets at birth from index selection was occurred, followed by an additional increase of 1.4 piglets during direct litter size selection. Santacreu et al. (2005) suggested selection for uterine capacity and direct selection for litter size in rabbits also would increase litter size. Rosendo et al. (2007b) reported that selection for prenatal survival increased pigs born alive by 0.2 per generation. The Wilson reference was removed as there is a serious scientific flaw with that paper.

Selection for ovulation rate in pigs was effective (Zimmerman and Cunningham, 1975; Blasco et al., 1998; Ruiz-Flores and Johnson, 2001) but resulted in only small response in litter size (Cunningham et al., 1979; Christenson et al., 1987; Lamberson et al., 1991; Rosendo et al., 2007a), even less response than direct selection for litter size (Johnson et al., 1984; Bennett and Leymaster, 1989, 1990b). Ovulation rate is quite highly heritable (~40%), and responded well to selection. However, embryo survival and fetal survival decreased and numbers of stillborn and mummified pigs increased (Cunningham et al., 1979; Johnson et al., 1999; Ruiz-Flores and Johnson, 2001; Petry and Johnson, 2004). Decreased embryo survival and fetal survival is thought to result from uterine overcrowding (Dziuk, 1968; Webel and Dziuk, 1974), and to be effective, selection for ovulation rate must be accompanied by selection for increased uterine capacity, particularly during the later stages of gestation, to result in increased live pigs per litter at birth.

Increasing litter size would be expected to decrease piglet birth weight and decrease piglet survival (Roehe, 1999; Arango et al., 2005a; Canario et al., 2006b; Rosendo et al., 2007b). Rosendo et al. (2007b) showed that piglet birth weight is generally negatively correlated with piglet birth survival and piglet birth to weaning survival.

Several studies have reported that growth rate and backfat depth have small genetic correlations with litter size (Young et al., 1977, 1978; Fredeen and Mikami,

1986b; Cleveland., 1988; Estany et al., 2002; Noguera et al., 2002; Chen et al., 2003; Holl and Robison, 2003; Petry et al., 2004; Arango et al., 2005a; Rosendo et al., 2007c). Long-term selection for productive traits, however, may result in significant effects on reproductive traits (Chen et al., 2003; Arango et al., 2005a) and long-term selection for litter size may result in significant effects on lean growth (Estany et al., 2002). This study includes results of selection on number of pigs born alive, and weight, backfat, and longissimus muscle area at 180 d during the last eight generations of a 28-generation selection experiment.

Most experiments reported in the literature involved short-term selection with selection only for one trait or for one index in the selection line during the entire experiment. This study, however, will report on long-term selection for number of pigs born alive that included lines selected for indexes of ovulation rate and embryonic survival, ovulation rate and number of total born pigs, number of fully formed pigs, number of pigs born alive, and number of pigs born alive, 180 d weight, backfat and longissimus muscle area. Successful long-term selection for number of pigs born alive, in this Large White-Landrace composite population may already have resulted in satisfactory genetic responses in some selected traits. To determine whether to continue selection or to change selection strategy, the main goal of this study will be to determine whether number of pigs born alive has reached a selection limit (response plateau). The second goal is to investigate whether responses are

affected when number of pig born alive and post-weaning traits are included in the selection objective. The third goal is to investigate the nature of responses and correlated responses for each line over all generations and relationships among the traits. The study will combine data (16 traits) from 28 generations from all selection and control lines to

1) Estimate genetic parameters (variances, heritability and correlations) among the traits,

2) Estimate direct and correlated responses for each line by generation for all traits,

3) Investigate fitness (linearity or quadratic) genetic trends for all selected traits,

4) Estimate inbreeding effects for all traits and maternal effects for pre-weaning traits, post-weaning traits and number of weaned pigs, and

5) Determine whether genetic variance in these relatively small selection lines has been reduced.

Results will be discussed for three types of traits:

1) Reproductive traits; number of born alive pigs, number of total pigs born, number of stillborn pigs, number of mummified pigs, ovulation rate,

number of embryos, embryo survival rate, age of puberty, number of weaned pigs,

2) Pre-weaning traits; birth weight, weaning weight, litter birth weight, litter weaning weight,

3) Post-weaning traits (carcass traits); 180 d weight, 180 d backfat and 180 d longissimus muscle area.

Chapter 2

Literature Review

For swine, mice and rabbits, several studies show that reproduction can be improved by selection for ovulation rate, uterine capacity, embryo survival, fetus survival, litter size and placenta or an index selection of two or three of those reproductive traits. Growth can be improved by selection for measures of growth traits such as average daily gain, weight at specific ages, or ages to specific weights. And, carcass traits can be improved by selection for various measures of carcass lean such as backfat thickness and long muscle area. The interactions among selection for reproduction, growth rate and carcass traits were also reported.

Simulated models and suggested selection traits:

Dziuk (1968) used 130 gilts to investigate whether number of embryos and length of uterus affect embryo survival. Gilts were assigned to nine treatment groups: 1) normal; 2), 3) and 4) ligated uterus at 1/3 (1/3 of uterine size), 2/3 (2/3 of uterine size) or 1/2 (1/2 of uterine size) of distance between left and right oviduct; 5) ligation of one oviduct; 6) ligation of one uterin horn and one ovary; 7) injected pregnant mares serum gonadotrophin for inducing superovulation (less than 20 corpora lutea); 8) injected pregnant mares serum gonadotrophin for inducing superovulation (more than 20 corpora lutea); and 9) similar number of fertilized eggs implanted from donor

gilts. Embryo survival before 25 days of gestation was similar for any size of uterus with similar number of embryos. Within similar uterine size, embryo survival did not meaningfully decrease until embryos were more than 14. They guessed that uterine overcrowding may reduce embryo survival during earlier gestation.

Pope *et al.* (1972) used 36 crossbred recipient gilts to investigate whether number of embryos affects embryo survival. The recipient gilts were implanted with 12 or 24 ova from donor gilts at 24 ± 4 hour ovulation. The 332 transferred ova included 21.1% with single-cell ova, 68.2% with two-cell ova and 10.5% with four-cell ova. At 25 d of gestation, the gilts that received 24 ova had significantly ($P < 0.01$) larger litter size than the gilts that received 12 ova (17 vs. 7 embryos per litter) but embryo survival was not significantly different between the gilts that received 24 ova gilts (67.0%) and the gilts that received 12 ova (56.7%). Uterine overcrowding was shown to not be the main reason for litter size restriction during the 25 d of gestation.

Webel and Dziuk (1974) used 251 crossbred gilts to investigate whether uterine capacity affects prenatal survival at 25 - 30 d, 31 - 40 d and 41- 112 d of gestation. The gilts were grouped 1) half the normal size of uterus with injected pregnant mares serum gonadotrophin to induce superovulation); 2) normal size uterus for each embryo; 3) twice the normal size of uterus (ligated one oviduct). Embryo survival at any period of gestation was not significantly changed by number of

embryos in the normal size uterus. But, embryo survival after 30d of gestation decreased in half the normal size of uterus. They thought large number of fetuses or restricted uterus may be one of reasons fetuses died after 30 d of gestation.

Bennett and Leymaster (1989) simulated (n = 20,000) a swine model for litter size based on ovulation rate, potential embryonic viability and uterine capacity (the number of fetuses that dam's uterus can nurture from time of ovulation until birth). Based on experimental results reported by others, mean and standard deviation of ovulation rate and potential embryonic viability in the model were set at 12.69 ± 2.58 ova and 0.74 ± 0.18 pig/ova. Initial mean and standard deviation of uterine capacity were 11.98 ± 4.20 pigs, but mean and standard deviation of uterine capacity were changed every generation until simulated mean and standard deviation of litter size were the same as experimental results. Heritability was set at 0.25 for ovulation rate and at 0.15 or 0.20 for uterine capacity. Ovulation rate and uterine capacity were simulated by standard normal distribution. After multiplication by their own standard deviations and adding mean ovulation rate and uterine capacity, simulated sampled ovulation rate and uterine capacity were set at an integer value (1 included values less than 1). Viability of sampled embryo (x) was simulated by binomial distribution with ovulation rate (n) and proportion of potential embryonic viability (p), i.e., $P(x) = \frac{n!}{x!(n-x)!} \times p^x \times (1-p)^{n-x}$. The product of ovulation rate and embryo survival is litter size when uterine capacity is unlimited, but in the simulation, litter size was the

minimum number of simulated embryos and uterine capacity. Embryo survival was obtained by the ratio of litter size to ovulation rate. Litter size was simulated for 25 combinations of mean ovulation rate and uterine capacity in the simulated data. The correlation of ovulation rate and uterine capacity was small and independently changing ovulation rate or uterine capacity had limited changes on litter size. Their conclusion was that a single gene of hormonal control or nutritional control would not be effective to improve litter size. They suggested that combinations of genes and treatment controls may increase litter size.

Bennett and Leymaster (1990a) compared genetic models for representing genetic characteristics of a model of litter size based on ovulation rate, uterine capacity and embryonic viability. The litter size model included a combination of additive, additive × additive, additive × mean environment, additive × random environmental and random environmental effects of ovulation rate and uterine capacity. Results showed genetic correlations of litter size with ovulation rate and uterine capacity depended on means of ovulation rate and uterine capacity and that genetic interaction of means of ovulation rate and uterine capacity affect heterosis for litter size. They determined that the sum of genotype and environmental effects for litter size was a product of genotype plus environment effects for ovulation rate and embryo survival. They suggested that an associative effects model of ovulation rate and uterine capacity can be used to predict selection for litter size.

Bennett and Leymaster (1990b) reported responses to simulated weak (20 generations) and intense (10 generations) selection for ovulation rate, for uterine capacity, for embryo survival, for litter size, for an index of ovulation rate and uterine capacity, for an index of ovulation rate and embryo survival and for an index of ovulation rate and litter size. Inbreeding effects and (co)variance of temporary genetic disequilibrium effects were ignored in the model. Simulated weak selection was based on previous simulation of Bennett and Leymaster (1989). The initial means of ovulation rate and uterine capacity were 12.68 ova and 12.0 pigs. The combined selection differential for sires and dams was 0.2 phenotypic standard deviations per generation. Heritability was set at 0.25 for ovulation rate and at 0.20 for uterine capacity. Parameters were changed every generation for calculating expected genetic changes when relationships of parameters are nonlinear. For single-trait selection for litter size and uterine capacity, the simulated means of ovulation rate and uterine capacity were 16.68 ova and 16.0 pigs. For intense selection, each generation had about 1,000 litter records. Selection of males and females was based on their dam's phenotypic record. The average genotype of dams of replacement gilts was from the top 30% of selected females. The average genotype of dams of sires was the top 10% of selected females. Sample size of 25,000 was expected to reduce random error of litter size and embryo survival estimations at the final generation. Responses to weak selection and intense selection on ovulation rate, uterine capacity and embryo survival resulted in less litter size (weak selection: 6%, 35% and 79%; intense selection: 26%,

67% and 103%) than direct litter size selection. However, responses from indexes of 3.16 ovulation rate plus uterine capacity, of 2.73 ovulation rate and uterine capacity, of 11.80 ovulation rate plus embryo survival and of 0.70 ovulation rate plus litter size resulted in greater litter size (weak selection: 37%, 37%, 21% and 21%; intense selection: 27%, 39%, 13% and 19%) than from direct litter size selection. They concluded that selection for indexes of ovulation rate and litter size or for ovulation and embryo survival after selection for index of ovulation rate and uterine capacity can gain the most litter size. Direct selection for litter size increased litter size more than independent selection for ovulation rate, uterine capacity or embryo survival, but litter size increased less than from an index of ovulation rate and uterine capacity, an index of ovulation rate and embryo survival or an index of ovulation rate and litter size.

Pérez-Enciso and Bidanel (1997) discussed possible causes of the contradictious between theoretical prediction and experimental results of selection for litter size components. Theoretical prediction was based on Bradford (1980): ”direct selection on litter size is the remarkable effective way to improve total born pigs per litter” and index theory (Falconer and Mackay, 1996). The value of index selection for ovulation rate and litter size to direct selection on litter size is:

$$\sqrt{1 + (\text{covariance of ovulation rate and litter size})^2 \times (\frac{\text{heritability of ovulation rate}}{\text{heritability of litter size}})}.$$

Their review of the literature was focused on selection for ovulation rate, for

an index of ovulation rate and litter size and for an index of ovulation rate and prenatal survival. From theory of index selection, they predicted litter size response from index selection for ovulation rate and litter size to direct selection on litter size is about 1 when genetic variance of litter size equals the covariance between ovulation rate and litter size. With mass selection, expected total litter size response would be [1 + (phenotypic variance of litter size/phenotypic variance of ovulation rate)]$^{1/2}$. They suggested genetic drift to be one explanation for differences between theoretical expectation and experimental results in the literature. They guessed that large experimental size required may be a reason why direct selection on litter size did not extensively apply to animal breeding programs may be.

Wilson *et al.* (1999) used 12 Yorkshire sows to investigate whether placental size (PZ) and placental efficiency (PE = pig weight/placental weight) are heritable by measuring response of born alive pigs to groups of higher (H) or lower (L) than average placental efficiency. Both groups had similar body weight but the higher placental efficiency group had lighter placental weights than the lower placental efficiency group ($P < 0.01$). The high placental efficiency group produced more pigs born alive ($P < 0.05$), had lighter piglet birth weights ($P < 0.05$) and had lighter placental weights ($P < 0.01$) than the low placental efficiency group (H vs. L: 12.5 ± 0.7 vs. 9.6 ± 0.5 pigs, 1.2 ± 0.1 vs. 1.5 ± 0.1 kg and 250 ± 10 vs. 347 ± 15 g). Because both groups had similar body weight and the higher placental efficiency group had

lighter placental weight, the higher placental efficiency group had higher placental efficiency than the lower placental efficiency group. They suggested that selection for smaller placental size and higher placental efficiency may be a method for increasing litter size in swine. However, this study was for too small to produce selection genetic estimates.

Leenhouwers *et al.* (2003) investigated the relationship between breeding value of sows for farrowing survival and piglets for farrowing survival (n = 39,504, from 1998 to 2002) and incidence of stillborn pigs, fully formed pigs, pigs born alive, litter birth weight and variation in within litter birth weight. The 336 litters with stillborn pigs included non-fresh stillborn, pre-partum stillborn, intra-partum stillborn and post-partum stillborn pigs. Pigs born alive had significantly heavier birth weights than most kinds of stillborn pigs, except for pre-partum stillborn pigs ($P < 0.0001$). Increased breeding values for piglet farrowing survival would be expected to decrease number of non-fresh stillborn pigs ($P < 0.01$), number of pre-partum stillborn pigs ($P < 0.01$), number of post-partum stillborn pigs ($P < 0.01$) and also number of fully formed pigs ($P = 0.0003$). Number of intra-partum stillborn pigs, average litter birth weight and variation in within litter birth weight did not change. Increased breeding values for maternal farrowing survival would be expected to decrease all kinds of stillborn pigs ($P < 0.01$), average litter birth weight ($P = 0.05$) and variation in within litter birth weight ($P = 0.05$), but to not change number of fully formed pigs. The

relationship of number of stillborn pigs with breeding values for maternal farrowing survival was stronger than that with breeding values for piglet farrowing survival. They concluded that selection for maternal farrowing survival would be expected to decrease all kinds of stillborn pigs without affecting litter size and that the decreases would be greater than for piglet farrowing survival.

Long-term selection in mice:

Bakker *et al.* (1978) estimated the direct and correlated responses after 29 generations of selection based on top 24 largest litters at first parity in a large Swiss mouse population. The founder population was chosen as the largest 24 litters from approximately 1,000 litters of large Swiss randomly bred mouse breeding unit. Four females were chosen randomly from each of the largest 24 litters; 3 males were chosen randomly from each of the largest eight litters. At eight weeks of age, 4 females were randomly mated with one male. Therefore, each generation, there were 96 females by 24 males and replacements were selected from the 24 largest litters. The same selection policy was used and sib mating was avoided for 29 generations. Over 29 generations, heritability estimates for litter size did not significantly change. Realized heritability for litter size was 0.11 ± 0.01 ($P < 0.01$). Total selection response for litter size was 6 young (14 young born at generation 29). Correlated responses for mortality rate at 0-12 d of age and 12-21 d of age and for body weight at 21-56 d of

age were not significant, but mortality in the selection line (0.05 ± 0.03 young) was greater than in the control line at 0-12 d of age (-0.03 ± 0.01 young). The study showed that selection for increased ovulation rate increased litter size. When females exposure less days to male during puberty ($P < 0.01$), females can produce more litters ($P < 0.01$). They concluded that selection for large litter size improved litter size at birth, although realized heritability was low, and did not change mortality, body weight and other reproductive traits.

Bradford (1979) reported experimental results from one control line and selection line for large and for small litter size from the same founder mice population. He analyzed genetic variation in litter size and litter size components (ovulation rate and prenatal survival) for 51 generations. Selection for ovulation rate increased litter size but decreased embryo post-implantation survival. Long-term selection for ovulation rate with high inbreeding also increased prenatal survival, but did not produce maximum response on prenatal survival. Because large genetic variation for prenatal survival existed, likely due to recessive alleles that causes mice to die. Direct selection for prenatal survival increased prenatal survival and litter size but decreased embryo pre- and post-implantation survival. Variation in dam's genotype was the main effect to cause the selection differentials. Variation in embryo survival genotype also contributed, but was less than dam's genotype. Variation in both fertility and prenatal survival were mainly due to dominant genes. Variation in ovulation rate and

body weight was mainly due to additive genes.

Barria and Bradford (1981a) used records from three other selection lines and a continued control line (LC) to analyze whether genetic variance remained after long-term selection (33 generations in mice) for rapid post-weaning gain which had probably reached a selection limit. The three selection lines, derived from a post-weaning gain selection line (LS), included a selection line for slow gain (LA, generations 33-43), a relaxed selection line for rapid gain (LB, generations 34-43) and a relaxed selection line for rapid gain with inbreeding (LC, generations 34-43). After ten generations, there were almost no responses in LS (b = 0.03 ± 0.07 g/generation, realized heritability = 0.02 ± 0.05) but in LA gain decreased (b = -0.75 ± 0.07 g/generation) with realized heritability of 0.24 ± 0.03. These results showed that additive genetic variance still existed in LA after initial selection for 33 generations. Gain in LB (b = -0.32 ± 0.07 g/generation) and LC (b = -0.42 ± 0.07 g/generation) decreased. LC result showed there was little heterosis and inbreeding did not help break the selection limit. They suggested additive genetic variance for post-weaning gain had not been exhausted because a negative association between post-weaning gain and fitness was the cause of the selection limit.

Barria and Bradford (1981b) in other analysis of Barria and Bradford (1981a) focused on correlated genetic changes in fertility, litter size components (ovulation rate and embryo survival), productivity and estimates of correlations among these

reproduction traits and growth. Fertility in LS tended to decrease but with significant undulation between generations over the 43 generation. When growth rate decreased, fertility was restored in LA much faster than in LB. Fertility, however, in LC also decreased. In LC large heterosis (dominance) effects were found for fertility and litter size but only a little for growth rate. They concluded that considerable residual genetic variation still existed in growth and reproduction traits in LA, and that selection limit in LA was reached because of negative genetic correlation between fitness and post-weaning gain. Selection for rapid post-weaning gain resulted in large and negative correlated change in fertility.

Relationship between reproduction traits and growth traits:

Young *et al.* (1977) estimated the phenotypic and genetic correlations among pre-breeding traits and reproductive traits at about 30 d of gestation for records from 126 Duroc, 130 Hampshire and 83 Yorkshire purebred gilts and 192 two-breed cross gilts from the Oklahoma swine crossbreeding project. Number of corpora lutea (ovulation rate) had moderate to high positive genetic correlations with individual birth weight (kg, r_g = 0.42), individual weaning weight (kg), litter weaning weight (kg, r_g = 0.41), average daily gain at 100 kg (kg/d, r_g = 0.79), breeding weight (kg, r_g = 0.49) and days from 100 kg to breeding (d, r_g = 0.69) and high negative genetic correlations with age at 100 kg (d) and litter age at 100 kg (d, r_g = -0.73). The ratio of

ovulation rate to number of live embryos was highly correlated genetically with individual birth weight (kg, r_g = -0.90) and individual weaning weight (kg, r_g = 0.91). Estimates of phenotypic correlations between ovulation rate and average daily gain at 100 kg (kg/d), age at 100 kg (d), litter age at 100 kg (d), breeding weight (kg) and days from 100 kg to breeding (d) were significantly different from zero (r_g = 0.21, -0.16, -0.15, 0.27 and 0.18, respectively). Estimates of phenotypic correlations between number of live embryos (NE) and litter age at 100 kg (d), breeding weight (kg) and breeding age (d) were significant (r_g = -0.07, 0.17 and 0.20, respectively). Small variation in ovulation rate, number of embryos, embryo per corpora lutea and corpora lutea per embryo were predicted by regression on pre-breeding traits (R^2 = 14.6%, 17.7%, 9.1% and 6.3%, respectively). Results indicated that gilts that grow faster will have greater ovulation rate but may have lower embryo survival. Older and heavier gilts at breeding have greater ovulation rate and more embryos. Gilts with heavier birth weight had more embryos survive, but gilts with heavier weaning weight had less embryos survive. Pre-breeding traits explained only small proportion of the variation in reproduction traits at 30 d of gestation.

Young *et al.* (1978) estimated heritability and phenotypic and genetic correlations for 25 pre-breeding traits and six reproduction traits from records of 2,095 gilts in the University of Nebraska Gene Pool population. Estimates of phenotypic and genetic correlations among pre-breeding growth traits were positive

(r_p = 0.20~0.89, r_g = 0.23~1.14) but only phenotypic correlations were significant (P < 0.01). Estimates of heritability (diagonal) and phenotypic (lower diagonal) and genetic (upper diagonal) correlations among ovulation rate (OR), number of fully formed pigs, number of born alive pigs (BA), number of pig weaned (NW), litter birth weight (LBW) and litter weaning weight at about 42 d (LWW) for first litters were:

Trait	OR	FF	BA	NW	LBW	LWW
OR	**0.59**	-0.01	-0.38	-1.53	-0.88	-1.29
FF	0.06	**0.72**	0.96	0.76	1.03	0.59
BA	0.04	0.93	**0.66**	0.80	0.92	0.56
NW	0.02	0.74	0.83	**0.29**	0.64	0.95
LBW	0.05	0.76	0.84	0.80	**0.29**	0.55
LWW	0.02	0.62	0.71	0.91	0.80	**0.38**

Reproduction traits had moderate to high estimates of heritability. Estimates of genetic correlation among all reproduction traits were not significantly different from zero with large standard errors (0.33 ~ 1.18). Estimates of phenotypic correlations of ovulation rate with other reproduction traits were positive, small and not significant. Estimates of phenotypic correlation among litter size traits were significantly positive and large (P < 0.01). Estimates of phenotypic correlations between litter size traits (FF, BA and NW) and litter weight (LBW and LWW) traits were significantly positive and large (r_p = 0.62 ~ 0.93, P < 0.01). Estimates of phenotypic correlations between ovulation rate and pre-breeding growth traits at weaning (about 24 d of age), at 140 d of age, at puberty and average daily gain from 42 to 140 d of age were significant, moderate and positive (P < 0.05). Estimates of phenotypic correlations of pre-breeding traits with litter size traits and litter weight traits were small and not

significant. The correlation between ovulation rate at second estrus and litter size was small, but ovulation rate and the pre-breeding growth traits had a moderately positive correlation. The pre-breeding growth traits affected litter size traits slightly.

Estany *et al.* (2002) used records of Landrace pigs from the Nova Genètica breeding farm in Spain to estimate correlated responses to selection for litter size, for body weight from 30 to 165 d of age (n = 1,939), backfat thickness from 135 to 165 d of age (n = 636) and daily feed intake from 75 to 165 d of age (n = 11,959). The correlated responses showed body weights at 75 d ($P < 0.01$), 105 d ($P < 0.01$) and 135 d ($P < 0.05$) of age in the selected litter size line were slightly greater than in the control line, but body weight at 30 and 165 d of age were not significantly different between the two lines. Midback and loin backfat at 135 ~ 165 d of age in the selection line were significantly greater than in the control line ($P < 0.01$). Feed intake from 75 to 165 d of age in the selection line was a little greater, but not significantly different, from control line. Growth rate in the selected litter size line was greater at 30 d and 75 d of age ($P < 0.01$), but less at 165 d of age than in the control line. The selected litter size line at earlier ages also had slightly higher feed efficiency than the control line, but feed efficiency in the control line was slightly better at about 100 d to 165 d of age (differences less than 18 ± 6 g of weight gain/kg of feed consumption). After 185 kg of feed intake, feed efficiency over the test period in the selected litter size line was slightly greater than in the control line (differences was 1.37 ± 0.77 kg of weight gain,

P = 0.08). They suggested that long term selection for litter size may result in decreased lean growth because of increased fat deposition at an earlier age.

Holm *et al.* (2004) estimated genetic correlations between reproduction traits and production traits for Norwegian Landrace in nucleus pigs (1990 ~ 2000). Estimates of genetic correlations between reproduction traits [age at the first puberty (AP, d, n = 56,932), number of born alive pigs in the first parity (BA_1, pig, n = 36,102) or second parity (BA_2, pig, n = 19,243) and days from weaning to first puberty after first parity (WD_1, d, n = 25,168) or second parity (WD_2, d, n = 13,793)] and production traits [adjusted age at 100 kg (AGE, d, n = 190,454), percentage of lean content (PLC, %, n = 12,487), feed consumption from 25 to 100 kg (FC, kg, n = 12,992) and adjusted backfat thickness (BF, mm, n = 190,453)] and estimates of heritability (h^2) for traits were:

Traits	AP	BA_1	BA_2	WD_1	WD_2	h^2
AGE	0.68	0.60	0.42	0.16	0.20	0.30
PLC	0.02	-0.12	-0.24	-0.09	0.05	0.44
FC	0.20	0.23	0.20	0.04	0.01	0.22
BF	-0.03	0.00	0.08	-0.12	0.03	0.58
h^2	0.37	0.10	0.10	0.06	0.03	0.23

Decreased age at 100 kg, decreased feed consumption from 25 to 100 kg, or increased percentage of lean content would be expected to decrease number of pigs born alive. Decreased age at 100 kg or decreased feed consumption from 25 to 100 kg would be expected to decrease age at puberty. Decreased backfat thickness would be expected to have little effect on most reproductive traits (except for day from weaning to first

estrus after first parity). It was concluded that selection for favorable production traits, except for selection for decreased backfat, would be expected to result in unfavorable reproductive performance.

Arango *et al.* (2005a) used threshold-linear model analysis to estimate variance components and genetic relationships among number of piglets born dead (BD, n = 47, 454), number of piglets born alive (BA, n = 47,454), age to 113.5 kg (AD, n = 30,832) and average of backfat at the 10th and last ribs at end of test (BF, n = 29,829) for first parity of Large White sows. They also estimated the genetic relationship between number of piglets born dead and number of piglets born alive across Parities 1 (n = 46,629), 2 (n = 36,410) and 3 (n = 26,408). The model included fixed effects of contemporary groups and random additive genetic effects. Estimates of heritability (diagonal) and genetic (upper diagonal) correlations among BD, BA, AD and BF in first parity were:

Trait	BD	BA	AD	BF
No. of piglet born dead (BD, pig)	**0.09**	-0.04	-0.14	-0.14
No. of piglet born alive (BA, pig)		**0.09**	0.08	0.05
Age to 113.5 kg (AD, d)			**0.37**	-0.22
Ultrasound backfat (BF, cm)				**0.31**

The table shows that piglet mortality at farrowing had small negative correlations with pig born alive, age at 113.5 kg and average backfat thickness. The genetic correlations of pig born alive with age of 113.5 kg and backfat thickness were small. Age at 113.5 kg and backfat thickness were moderately correlated. Estimates of heritability (diagonal) and genetic (upper diagonal) correlations between number of BD and BA

for parities 1, 2 and 3 were:

Trait	BD1	BD2	BD3	BA1	BA2	BA3
BD in Parity 1 (BD1)	**0.09**	0.96	0.91	0.04	0.09	-0.10
BD in Parity 2 (BD2)		**0.10**	0.96	0.02	0.14	-0.05
BD in Parity 3 (BD3)			**0.11**	0.02	0.17	-0.04
BA in Parity 1 (BA1)				**0.09**	0.74	0.77
BA in Parity 2 (BA2)					**0.12**	0.95
BA in Parity 3 (BA3)						**0.12**

The table shows the heritability estimates for number of pigs born alive and number of pigs born dead in parities 2 and 3 were slightly greater than in parity 1. Number of pigs born alive and number of pigs born dead were highly correlated across parities. Estimates of genetic correlations between number of pigs born alive and number of pigs born dead were small within and across three parities. They concluded selection for increased litter size would decrease piglet survival at birth, decrease growth, and increase backfat thickness. Long-term selection for increased growth and decreased backfat may increase piglet mortality at birth slightly.

Chen *et al.* (2003) used bivariate REML analyses (REMLF90, Misztal, 2000) to estimate genetic correlations between lean growth rate and litter traits for U.S. Yorkshire (n = 251,296 and 361,300), Duroc (n = 75,262 and 154,833), Hampshire (n = 83,338 and 99,311) and Landrace (n = 53,234 and 71,097) pigs from National Swine Registry Swine Testing and Genetic Evaluation System (1990 ~ 2000). Estimates of genetic correlations among lean growth rate (LG), backfat (BF), loin muscle area (LMA), age to 113.5 kg (DAY), born alive pigs (BA), litter weight at 21d

of age (WW), and number of weaned pigs (NW) and estimates of heritability (h^2) for all traits in 4 breeds were:

Traits	BA, pig	WW, kg	NW, pig	h^2
LG, kg/d	-0.11 ~ -0.09	-0.07 ~ -0.05	-0.007 ~ 0.004	0.37 ~ 0.45
BF, cm	0.18 ~ 0.19	-0.27 ~ -0.30	0.005 ~ 0.007	0.36 ~ 0.43
LMA, cm^2	-0.03 ~ 0.02	-0.05 ~ 0.08	-0.015 ~ -0.012	0.47 ~ 0.50
DAY	-0.07 ~ 0.05	-0.10 ~ 0.08	-0.005 ~ 0.006	0.30 ~ 0.35
h^2	0.07 ~ 0.10	0.07 ~ 0.09	0.05 ~ 0.07	

Genetic correlations of lean growth rate with pigs born alive and with litter weight at 21d of age were small and unfavorable for all breeds. Backfat was favorably correlated with litter weight at 21d of age but unfavorably lowly correlated with pigs born alive. Maternal genetic effects in all breeds were small for all traits (the fractions of variance due to maternal genetic effects were: 0.00 ~ 0.05). They inferred that means of litter traits might decrease under long-term selection for lean growth rate.

Selection for placental traits:

Mesa *et al.* (2005) used 193 sows and their piglets to estimate variance components for piglet birth weight (BW, n = 2,111), placental weight (PW, n = 2,006), placental efficiency (PE = BW/PW, n = 1,677), fully formed pigs (FF) and to estimate responses to index divergent selection after four generations for placental efficiency (I = 0.073 FF+ 0.003 BW – 0.012 PW). Estimates of heritability (diagonal) and direct genetic (upper diagonal) and maternal genetic (lower diagonal) correlations among

traits were:

Traits	BW	PW	PE	I	FF
BW	**0.03**	0.60	0.06	-0.71	-0.33
PW	0.96	**0.25**	-0.95	-0.87	-1.00
PE	-0.66	-0.89	**0.18**	0.96	-0.63
I	-0.76	-0.55	0.91	**0.11**	-0.18
FF	-0.28	-0.98	0.12	-0.56	**0.08**

Piglet birth weight, placental weight, placental efficiency and the index were significantly correlated ($P < 0.001$). Additive and maternal genetic correlations between index and index traits were high. Maternal traits were not significantly correlated phenotypicaly with litter traits. After four generations, placental weight in the line selected for decreased placental efficiency was heavier than the line selected for increased placental efficiency ($b = 14.9 \pm 2.5$ vs. -5.8 ± 0.8 g/generation, $P < 0.001$). The positive genetic change of placental efficiency in the line selected for increased placental efficiency was greater than the negative genetic change in the line selected for decreased placental efficiency ($b = 0.14 \pm 0.00$ g vs. -0.09 ± 0.03 ratio, $P < 0.001$). However, genetic change of fully formed pigs in the line selected for increased placental efficiency was less than in the line selected for decreased placental efficiency line ($b = -0.02 \pm 0.02$ g vs. 0.05 ± 0.01 pigs/generation, $P < 0.01$). Unlike the results of Wilson *et al.* (1999) concluded that index selection for increased placental efficiency and decreased placental weight will not improve litter size. It did result in increased placental efficiency, but slightly decreased number of fully formed

pigs. They suggested index selection for birth weight, placental weight and litter size might be used to increase litter size with higher birth weight and pre-weaning survival.

Selection for uterine capacity:

Blasco *et al.* (2005) used a Bayesian analysis with Gibbs sampling to estimate heritability and correlated responses for reproductive traits from divergent selected for ten generations for uterine capacity (UC, measured by litter size,) from 735 unilaterally ovariectomized rabbits (four parities including 2,996 litters) of a White New Zealand - Californian crossbred population. Estimates of heritability (diagonal) and phenotypic (lower diagonal) and genetic (upper diagonal) correlations of uterine capacity with ovulation rate (OR, n = 735), implanted embryos (IE, n = 735) at 12 d of the second estrus, embryo survival (ES = IE/OR), fetal survival (FS = UC/IE) and prenatal survival (PS = UC/OR) were:

Traits	UC	OR	IE	ES	FS	PS
UC	**0.11**	0.56	0.66	0.64	0.24	0.53
OR	0.33	**0.32**	0.91	0.61	-0.63	-0.37
IE	0.57	0.08	**0.22**	0.55	-0.68	-0.35
ES	0.54	-0.28	0.80	**0.04**	-0.09	-0.21
FS	0.57	-0.19	-0.31	-0.19	**0.14**	0.90
PS	0.89	-0.36	0.37	0.62	0.62	**0.09**

The difference between lines at generation ten was 1.5 rabbits. The first generation contributed about 50% of the difference in response. They suggested that a major

gene may have been segregating in the base population. They concluded that the response to selection for uterine capacity in this study was similar to that of direct selection for litter size in other studies. They suggested that measurement from a single uterine horn may be a good measure of uterine capacity for both intact uterine horn (two horns) and a good measure of correlated response for litter size.

Santacreu *et al.* (2005) used a Bayesian analysis with Gibbs sampling to estimate correlated responses of reproductive traits to selection for litter size from measurement of 294 intact females at the 11^{th} and 12^{th} generations of the selection experiment described (divergent selected for uterine capacity (UC) in unilaterally ovariectomized rabbits) by Blasco *et al.* (2005). They also investigated whether response for litter size was symmetric for the high UC line (H) and low UC line (L) using a cryopreserved control line (C). The correlated responses for litter size were not symmetric for high UC line and low UC line because low UC line, which had lower prenatal survival (PS), had greater correlated responses for litter size than high UC line, which had higher prenatal survival (C-L vs. H-C: LS = 1.88 vs. 0.47 pigs and PS = 0.14 vs. 0.05). The low UC line also had a larger decrease in embryo survival (ES) and fetal survival (FS) than the high UC line (C-L vs. H-C: ES = 0.10 vs. 0.00 and FS = 0.08 vs. 0.04), which would explain the smaller response for litter size in the low UC line. They concluded that selection for high uterine capacity and direct selection for litter size resulted in similar increase in prolificacy. Change in embryo

survival and fetal survival explained the correlated response for litter size.

Selection for ovulation rate and/or embryo survival:

Zimmerman and Cunningham (1975) estimated response to selection for ovulation rate (845 selection line and 845 control line gilts) from five generations in the University of Nebraska Gene Pool population. The inbreeding coefficient of this composite population (14 different breeds) was similar in both selection (0.89%) line and control line (0.88%). The ovulation rate of the selection line increased 0.40 ± 0.09 per generation (16.2 ova at generation five) but the ovulation rate of control line decreased 0.16 ± 0.05 per generation (13.7 ova at generation five). Realized heritability was 0.52 ± 0.01, 0.40 ± 0.08 and 0.45 ± 0.07 from regression of response on cumulative selection differential, from regression of the selection - control line difference on weighted cumulative selection differential and from the fifth generation, respectively. Selection for increased ovulation rate was effective.

Cunningham *et al.* (1979) reported correlated responses to selection for increased ovulation rate for fully formed pigs (FF), pigs born alive (BA), number of pigs weaned (NW), litter birth weight (LBW) and litter weaning weight (LWW) for 387 selection line and 394 control line litters after nine generations of selection from the same base composite population as Zimmerman and Cunningham (1975).

Realized heritability for ovulation rate was 0.42 ± 0.06 from regression of the selection - control line difference on weighted cumulative selection differential. Estimates of genetic correlations of ovulation rate with FF, BA, NW, LBW and LWW were 0.07, 0.11, 0.24, 0.18 and 0.20, respectively. Regression of average correlated response on generation was significant only for LBW of both selection (b = -0.31 ± 0.12 kg/generation) and control lines (b = -0.41 ± 0.06 kg/generation) and for LWW of control line (b = -3.4 ± 0.08 kg/generation). Regression of average correlated response of differences in lines was not significant for all litter traits and litter weight traits, but for ovulation rate was significant in generation 9 (selection line – control line = 3.71 ova). Decreased fertilization rate and/or embryo survival was thought to be the cause(s) of lack in correlated response in litter size and litter weight traits.

Christenson *et al.* (1987) used records of crossbred Yorkshire × Landrace × Chester White × Large White) gilts to estimate differences in ovulation rate, postnatal survival and litter size between 110 uniltaterally hysterectomized-ovariectomized (UHO) gilts (surgery after first estrus of 8 ~ 12 d) and 142 intact ovary gilts. They found UHO gilts (11.9 ova) ovulated a similar number of ova as intact gilts (12.1 ova) measured at 40 d of gestation. Intact gilts, however, produced significantly larger litters at birth than UHO gilts (9.0 ± 0.3 vs. 5.7 ± 0.3 pigs, $P < 0.01$). Estimates of regression coefficients of litter size (number of fully formed pigs) on ovulation rate for UHO and intact gilts at 86 d of gestation, at farrowing and averaged over time

were:

	Regression coefficients (fully formed pigs/number of corpora lutera)		
	At 86 d of gestation	At farrowing	Averaged over time
Intact gilts	0.60 ± 0.12	0.42 ± 0.14	0.51 ± 0.10
UHO gilts	0.41 ± 0.15	0.07 ± 0.17	0.24 ± 0.12

The UHO gilts had more fetal losses and lighter piglet birth weights than intact gilts. Weight and litter size to 14 d of age, postnatal survival and average daily gain were similar for both intact and UHO gilts. They concluded that ovulation rate and litter size were almost independent for both intact and UHO gilts. Use of ovulation rate to estimate uterine capacity would not be recommended.

Neal *et al.* (1989) estimated genetic parameters and responses after five generations of selection for an index of ovulation rate (OR) and embryo survival (ES = fetuses/OR, %) at 50 d of gestation (I = 10.6 × OR + 72.6 × ES) for a population of Large White and Landrace composite pigs. On average, 43 litters were produced by 18 sires in the selection line each generation. On average, 42 litters were produced by 15 sires in control line each generation. All females (average of 147) in selection line, but 50% of females in control line were laparotomized for counting number of corpora lutea and fetuses (F, pigs). Average inbreeding coefficients at Generation five for selection and control lines were 0.0534 and 0.0459. Regression of line differences on generation for OR, F, ES and I at 50 d of gestation were 0.57 ± 0.11 ova ($P < 0.01$), 0.20 ± 0.20 pigs, 1.30 ± 0.96% and 5.1 ± 1.76 ($P < 0.05$), respectively. Heritability estimated by regression of gilt on dam for OR, F and ES were 0.17 ± 0.07, 0.08 ± 0.10

and 0.18 ± 0.09, respectively. For I, realized heritability (0.30 ± 0.09) was higher than heritability estimated by regression of gilt on dam (0.12 ± 0.09). Estimates of genetic correlation of OR with F (-0.52 ± 0.40) and ES (-0.56 ± 0.24) were negative, but F and ES had a large genetic correlation (0.77 ± 0.23). They reported that the correlated response of litter size was 0.19 ± 0.14 pigs per generation (not significant). They suggested more investigation to estimate variance components and relationship among ovulation rate, embryo survival and uterine capacity for selection to improve litter size.

Blasco et al. (1998) used a Bayesian inference method to estimate genetic parameters and responses after four generation of selection for ovulation rate (OR) at 10~15 d of gestation or prenatal survival (PS) for the first two parities from records of 50 French Large White Sows farrowing each generation. Depending on priors, heritability estimates were 0.32 to 0.39 for ovulation rate and 0.11 to 0.16 for prenatal survival. Average response per generation was an increase of 0.38 to 0.40 ova for ovulation rate and 1.1 to 1.3% for prenatal survival. The study showed selection for litter size components (OR and PS) improved ovulation rate, that had high heritability, and increased prenatal survival slightly.

Johnson *et al.* (1999) used 14 generations of Large White - Landrace composite population to estimate differences in ovulation rate (OR), embryo survival, and litter traits between lines selected for increased litter size (L2) and a randomly

selected control line (L1). The population of the first five generations is the same as Neal *et al.* (1989).The first eleven generations were selected for increased index of ovulation rate and embryo survival and then the following three generations were selected for increased litter size. Ten different traits from 15,274 pigs were analyzed in this study. Number of fetuses at 50 of gestation (NF), total pigs born (TB), number of pigs born alive (BA) and ovulation rate were greater for L2 than for L1. Differences (L2 - L1) at Generation 11 were 3.8 pigs ($P<0.01$), 2.3 pigs ($P<0.01$), 1.1 pigs ($P<0.05$) and 7.4 ova ($P<0.01$) for NF, TB, BA and OR, respectively. Differences (L2-L1) at Generation 14 were 3.0 pigs ($P<0.01$) for TB and 1.4 ($P<0.05$) pigs for BA. A significant genetic relationship showed that when ovulation rate and number of fetuses at 50 d of gestation increase, number of stillborn pigs per litter is expected to increase.

Ruiz-Flores and Johnson (2001) later estimated direct and correlated responses from two - stage selection for ovulation rate (OR) and total pigs born (TB) for eight generations of the same base population as Johnson *et al.* (1999). The results provided evidence that total pigs born was improved by two - stage selection for OR and TB. Before two-stage selection (at Generation 8), average response of OR and TB for a selection line derived from L2 (L4) were a litter greater than for a selection line derived from L1 (L5) and a control line derived from L1 (L6). At Generation 8, previous responses of OR and TB were 4.24 ± 0.38 ova and 1.97 ± 0.39 pigs in L4,

and were 4.14 ± 0.29 ova and 1.06 ± 0.38 pigs in L5 and L6. After two-stage selection in both traits, the mean EBV from the last generation of L4 was greater than for both L5 and L6; the mean EBV in L5 was greater than L6. For OR, the mean EBV differences between L4 and L6, L4 and L5 and L5 and L6 were 6.20 ± 0.29, 3.94 ± 0.26 and 2.26 ± 0.29 ova, respectively. For TB, the mean EBV differences between L4 and L6, L4 and L5 and L5 and L6 were 4.66 ± 0.38, 1.86 ± 0.39 and 2.79 ± 0.39 pigs, respectively. The results showed two - stage selection for ovulation rate and total pigs born increased litter size and litter birth weight but decreased age at puberty.

Petry and Johnson (2004) estimated responses to selection for reproductive traits from 850 pure line and crossbred litters from three generations (Generation 17-19) of the same base population. The pure line, which included index lines (L4 and L5) and control line (L6), had 224 litters. The females of the pure lines were mated with Danbred NA Landrace (DL) boars and Duroc-Hampshire (DH) (3/4 Duroc and 1/4 Hampshire) terminal boars to produce the 393 F_1 litters. The DH males were mated with F_1 females to produce 233 three-way cross litters. The study showed total pigs born (TB), number of pigs born alive (BA), number of mummified pigs (MUM) and litter birth weight (LBW) were greater for L4 and L5 than Line 6, but weaned weight (WW) was greater for L6 than L4 and L5 ($P < 0.05$). Genetic differences between average of L4 and L5 and L6 were 3.53 pigs, 2.53 pigs, 0.22 pigs, 2.14 kg and 1.88 kg for TB, BA, MUM, LBW and WW, respectively. Crossbreeding pigs in

index line had significant improvement in TB, SB, number of weaned pigs and litter weaning weight.

Petry *et al.* (2004) estimated response in growth and carcass traits for 196 pure line and crossbred pigs from three generations of the same mating design as Petry and Johnson (2004). This result showed crossbred pigs had statistically greater longissimus muscle area (LMA), consumed more feed (CF), gain more body weight/consumed feed (GF), had better color score of LMA after 24 hours (LAC) and more lean with less BF than pure line pigs ($P < 0.05$). Differences in direct genetic value between crossbred and pure line pigs for LA, CF, GF, LAC, lean, BF and GR were 5.74 ± 0.926 cm^2, 0.23 ± 0.04 kg/day, 0.052 ± 0.005 kg/kg, 5.74 ± 1.377, 6.21 ± 0.90%, 0.89 ± 0.089 cm and 0.20 ± 0.016 kg/day, respectively. They concluded selection for growth and carcass traits may not increase or decrease litter size because of genetic small correlation between litter size and growth and carcass traits.

Rosendo *et al.* (2007a) estimated response to selection for ovulation rate (OR, n = 2,004) or prenatal survival (PS, n = 1,676) from six generations of French Large White population. They found that OR at puberty (ORP, n = 2,004) and at fertilization (ORF, n = 1,866) had high genetic correlations ($r_g > 0.72$). ORP had a small negative genetic correlation with PS, but a near zero estimate with PS corrected for OR (CPS = PS + 0.018ORF, n = 1,676). ORF was moderately negatively correlated with PS and CPS. Genetic trends per generation for ORP and ORF averaged 0.49 and 0.43 for the

line selected for OR, and 0.11 and 0.11 for the line selected for PS. Realized heritability of ORP was highly significant ($P < 0.001$). Total pigs born per litter (n = 1,798) had a moderately positive correlation with OR and correlations with PS and CPS were larger. They concluded that selection on ovulation rate improved ovulation rate without increasing litter size and that selection for prenatal survival or an index of ovulation rate and prenatal survival may be effective for improving total pigs born per litter.

Rosendo *et al.* (2007b) also estimated genetic parameters for litter traits and their direct and correlated responses to selection for OR or PS from the same population as Rosendo *et al.* (2007a). Litter size traits (LS, n = 1,798), which included number of pigs born alive (BA), weaned pigs (NW) and nurtured pigs (NNS) per litter, had high genetic correlations ($r_g = 0.95 \sim 0.99$). LS was negatively genetic correlated with average body weight (AW, n = 1,782, kg) at birth, at 21 d and at weaning age ($r_g = -0.46 \sim -0.19$) but was positively correlated with litter weight (LW, n = 1,782, kg) at birth, at 21 d and at weaning age ($r_g = 0.12 \sim 0.81$), OR ($r_g = 0.36 \sim 0.42$) and PS ($r_g = 0.75 \sim 0.78$). OR ($r_g = -0.26 \sim -0.21$) and PS ($r_g = -0.51 \sim -0.41$) were negatively genetic correlated with AW at birth, at 21 d and at weaning age. PS was negatively correlated with proportion of stillborn pigs (PSB, n = 1,798; $r_g = -0.33$). Proportions of stillbirth pigs (PSB, n = 1,798) were correlated negatively with LS ($r_g = -0.75 \sim -0.59$) and LW ($r_g = -0.44 \sim -0.17$), but positively with PSW ($r_g = 0.12$) and AW ($r_g = 0.12 \sim 0.30$). Significant ($P < 0.05$) genetic responses (selection line – control line)

per generation for age and weight at puberty averaged 2.1 d and 2.0 kg for the line selected for OR, and 3.2 d, 1.8 kg, and 0.2 pigs BA for the line selected for PS. The line selected for PS was different for LW at birth and AW at weaning by 0.21 pigs/generation and -0.25 kg/generation from control line ($P < 0.10$). They concluded direct or indirect selection on the components of litter size (OR and PS) improved litter size at birth but decreased pre-weaning survival. An index for selection for improving the number of piglets should include (an) additional trait(s) favorably related to farrowing and birth to weaning survival.

Rosendo *et al.* (2007c) also estimated genetic parameters and correlated responses for pre- and post-weaning growth and backfat thickness after selection for OR or PS from the same population as Rosendo *et al.* (2007a). For the OR line, the estimates of genetic correlations of OR with individual body weight (kg) at 3 week (I3WBW, n = 9,006), individual body weight at weaning (IWW, n = 9,114), ADG (g/d) from birth to weaning (ADGBW, n = 9,114), for ADG from 25 to 90 kg (ADGT, n = 8,267) and average backfat thickness (ABF, n = 3,540, mm) were not significant, but the estimates of direct genetic correlations of OR with age (d) at about 90 kg (-0.23 ± 0.09, AGET, n = 8,408) and the estimates of maternal genetic correlations of OR with individual piglet birth weight (-0.28 ± 0.13, IBW, n = not reported) and ADG from weaning to about 90 kg (0.23 ± 0.11, ADGPW, n = 9,021) were significant. For the PS line, the estimates of direct genetic correlations of PS with IBW, I3WBW, IWW, ADGBW, ADGPW, ADGT, ADET and ABF were low, but the estimates of maternal

genetic correlations of PS with body weight at birth (-0.65 ± 0.11), at 3 week (-0.56 ± 0.11) and at weaning (-0.59 ± 0.10) were high, and were moderate with ADG from birth to weaning (-0.34 ± 0.12) and ADG from weaning to about 90 kg (-0.20 ± 0.15). Maternal genetic change for individual piglet birth weight (-0.06 ± 0.02) was significantly reduced ($P < 0.05$). Direct genetic changes for ADG from 25 to 90 kg (n = 8,267) and age at about 90 kg were significantly improved in the OR line (4.1 ± 1.6 and -0.6 ± 0.2; $P < 0.05$) and in the PS line (7.8 ± 1.6 and -0.8 ± 0.2; $P < 0.001$). The conclusion was that selection for the components of litter size (OR or PS) slightly decreased birth weight and increased post-weaning growth (ADG from weaning to about 90 kg), but responses for direct genetic effects for growth rate and backfat thickness were small.

Selection for litter size:

Noguera *et al.* (2002) used Bayesian analysis with Gibbs sampler to estimate direct response and correlated responses of weight (WT, n = 24,426) and backfat thickness (BF, n = 24,426) at 175 d of age to selection for increased number of pigs born alive (BA, n = 66,620) for Landrace sows with six parities (1988 ~ 1998). Selection in the selection line was for the highest breeding values of 160 sows and 25 boars at the first generation only. In the following two generations in the selection line and in three generations of one control line, selection was random. At generation 1 in

the selection line, the result of BLUP repeatability animal model (heritability =0.06, accuracy = 0.13) showed the posterior mean for direct genetic responses for pigs born alive in parities 1 - 6 were 0.32, 0.43, 0.58, 0.64, 0.55 and 0.46, respectively. Correlated genetic responses of weight and backfat were low (WT: -0.66 kg and BF: 0.20 mm). They thought born alive pigs in different parities had different genetic background because of different posterior means for standardized selection differentials among parities. They concluded intense selection for increased number of pigs born alive increased number of pigs born alive but had little effect on weight and backfat thickness at 175 d of age.

Holl and Robison (2003) estimated heritability and direct and correlated responses to direct selection for number born alive pigs for nine generations by estimated breeding values with an animal model. Founder pigs (15 males and 32 females) were from the Nebraska control line of Large White and Landrace composite population. Each generation, about 15 males were mated with 60 females in selection line and about ten males mated with 30 females in control line. About ten or less selected females were reared in one pen. Realized heritability estimated using multiple regression for number born alive was 0.09 ± 0.08 in selection line and was 0.11 ± 0.166 in control line. The realized heritability estimate for number born alive was 0.13 ± 0.07 from regression of differences between selection line and control line on cumulative selection differentials. At generation nine, differences between

selection line and control line for number born alive pigs (0.86, $P < 0.05$), estimated breeding values (0.63, $P < 0.01$), and cumulative selection differentials were significant (9.05, $P < 0.01$), but differences for total born pigs, adjusted backfat and age of 104 kg were not significant. Estimated genetic and phenotypic changes per year for number born alive (BA, pigs/year), adjusted backfat (BF, mm/year) and age of 104 kg (AGE, d/year) in selection and control lines were:

Trait	Genetic trends		Phenotypic trends	
	Selection line	Control line	Selection line	Control line
BA	0.053 ± 0.002	-0.026 ± 0.004	0.145 ± 0.051	0.001 ± 0.085
BF	0.054 ± 0.013	0.026 ± 0.022	-0.012 ± 0.089	-0.043 ± 0.147
AGE	0.398 ± 0.110	-0.532 ± 0.182	0.307 ± 0.278	-0.519 ± 0.462

They concluded direct selection for number born alive pigs by estimated breeding values and reared 10 or less gilts in a pen improved number born alive and increased breeding values for adjusted backfat and age to 104 kg.

Selection for growth and carcass traits:

Fredeen and Mikami (1986a) estimated responses for three replicated lines to direct selection for rapid increased growth rate (Line G) and decreased backfat (Line B) and index selection of increased growth rate and decreased backfat (Line I) after nine generations of selection of Lacombe pigs (n = 992). Total variance of growth

increased 9% for females and 36% for males and total variance of backfat decreased 17% for females and 52% for males at last generation. The increase in growth rate in Line I was similar to that in Line G. The decrease in backfat in Line I was similar to that in Line B. Backfat increased in Line G as did growth rate. Growth rate decreased in Line B as did backfat. At the last generation, the net economic value in both traits for Line I was greater than for Lines G and B.

Fredeen and Mikami (1986b) estimated correlated responses for number and weight of fully formed pigs (FF), number of born alive pigs (BA), number of weaned pigs (NW) and piglet weight for the selection lines analyzed by Fredeen and Mikami (1986a) and for a control (C) line (n = 2,194 dams). Only Line I had significant increases in number and weight of fully formed pigs (b = 0.22 ± 0.05 pigs, $P < 0.01$ and 0.36 ± 0.07 kg, $P < 0.01$), pigs born alive (b = 0.11 ± 0.05 pigs, $P < 0.01$ and 0.29 ± 0.07 kg, $P < 0.05$) and weaned pigs (b = 0.14 ± 0.05 pigs, $P < 0.01$ and 3.81 ± 0.58 kg, $P < 0.01$) per generation. Line C had not significantly fewer fully formed pigs (b = -0.10 ± 0.05 pigs) and significantly fewer number of pigs born alive (b = -0.11 ± 0.05 pigs, $P < 0.05$) per generation. Piglet weight also decreased significantly for number of fully formed pigs (b = -0.17 ± 0.06 kg, $P < 0.01$) and for number of pigs born alive (b = -0.16 ± 0.06 kg, $P < 0.05$) per generation. After adjustment for line differences in inbreeding of dams, Line I had more pigs weaned than the other lines (Lines I > B > G > C) at generation nine.

Fredeen and Mikami (1986c) also estimated correlated responses for birth weight (BW, n = 16,284) and weaning weight (WW, n = 11,606) for the same selection lines and control line as analyzed by Fredeen and Mikami (1986a). Heritability estimates for birth weight and weaning weight were not significantly different from zero in all lines (BW = -0.03 ~ 0.07 and WW = 0.10 ~ 0.16). Only Line I had significant correlated responses for birth weight and weaning weight (b = 0.20 ± 0.10 g/generation and 0.28 ± 0.09 kg/generation, $P < 0.05$). They concluded selection for growth rate and/or backfat would have little effect on birth weight and weaning weight.

Fredeen and Mikami (1986d) estimated correlated responses in carcass traits for the same selection and control lines (n = 2,404 pigs) as Fredeen and Mikami (1986a). At generation 9, Lines G, B and I had significantly more lean content ($P < 0.05$) and less backfat ($P < 0.01$) than Line C. Line G had 10% greater daily gain ($P < 0.01$), 10% less backfat ($P < 0.01$), 2% more ham percentage ($P < 0.05$), 1% more predicted lean content ($P < 0.05$) but 2% shorter carcass length ($P < 0.05$) than Line C. Line B had 23% less backfat ($P < 0.01$), 3% bigger longissimus muscle area ($P < 0.05$), 2% longer carcass length ($P < 0.05$), 5% more predicted lean content ($P < 0.01$), 4% more ham percentage ($P < 0.01$) and 11% greater proportion of lean in ham face ($P < 0.01$) than Line C. Line I had 20% less backfat, 5% bigger longissimus muscle area and 12% more predicted lean content than Line C. Additional studies at

generation 12 showed Line I had better subjective color-structure and higher percentage of dissected lean from ham, loin and shoulder than Line C (Line I vs. C = 50.7 ± 0.7% vs. 46.1 ± 0.7%). They concluded selection for growth rate and/or backfat would increase growth rate and carcass lean content.

Bidanel et al. (1996) estimated genetic parameters and correlation among average daily gain between 30 and 85 kg (ADG, g/day, n = 3,664), average backfat thickness at 85 kg (ABF, mm, n = 3,664), age (AP, day, n = 1,919), weight (WP, kg, n = 1,919) and ovulation rate (OR, ova, n = 1,637) at first estrus, number of embryos (NE, n = 882) and embryo survival (ES = NE/OR, %, n = 882) at 30 days of gestation for 1,393 French Large White (LW), 110 French Landrace (LF) and 501 LW × LF gilts. LW gilts grew faster and were also fatter than LF (68 g/d, 2.6 mm) and LW × LF (28 g/d, 1 mm) gilts. LW × LF gilts were younger at puberty but were lighter in puberty weight than LW (-24.8 d, -18.4 kg) and LF (-7.7 d, 4.8 kg) gilts. At 30 days of gestation, LW gilts had more ova than LF (0.5 ova) and LW × LF (1.4 ova) gilts; LW × LF gilts had more embryos and greater embryo survival than LW (0.9 embryo, 8.8 %) and LF (0.9 embryo, 7.1%) gilts. Estimates of variance components were very similar for the three breeds (differences of less than 1%). Estimates of heritability (diagonal) and phenotypic (lower diagonal) and genetic (upper diagonal) correlations among traits for the Large White breed were:

Trait	ADG	ABF	AP	WP	OR	NE	ES
ADG	**0.24**	0.13	-0.18	0.34	0.20	0.18	0.06
ABF	0.28	**0.48**	-0.21	0.08	-0.09	-0.46	-0.56

AP	-0.16	-0.11	**0.29**	0.84	-0.36	-0.35	0.04
WP	0.26	0.07	0.66	**0.51**	-0.26	-0.18	0.18
OR	0.11	-0.02	-0.04	0.15	**0.27**	0.73	-0.11
NE	0.04	-0.06	0.00	0.13	0.37	**0.14**	0.79
ES	-0.04	-0.08	0.01	-0.03	-0.12	0.84	**0.08**

Their study showed there were negative genetic relationships between age and weight at puberty and reproductive traits. Selection for increasing growth would result in decreased age of puberty but selection for decreasing backfat would result in increased age of puberty. They concluded that the correlated responses for puberty traits to selection on an index of growth and backfat thickness would depend on economic values of growth and backfat thickness. They also concluded that the genetic variance components of litter size at 30 d of gestation, ovulation rate and embryo survival, were contributed mostly from the genetic variation in ovulation rate because the genetic variation in embryo survival was almost zero.

Cleveland *et al.* (1988) estimated correlated responses for reproduction and carcass traits from index selection for increased post-weaning ADG and decreased BF (I = 100 + 286.6 ADG - 39.4 BF) after five generations in University of Nebraska Gene Pool swine. Estimates of heritability (h^2), estimated from correlation among paternal half-sibs, realized genetic correlations between selection index and traits (r_g), and regression (b ± SE after adjusted genetic drift) of mean difference between lines (selection-control) on cumulative selection differential of index (b) per generation were:

Traits	h^2	r_g	b (unit/generation)
Fully formed pigs (n = 221, pig)	0.11	-0.24	-0.0033 ± 0.0026
Born alive pigs (n = 221, pig)	-	-	-0.0005 ± 0.002
Number weaned pigs (n = 221, pig)	0.03	-0.05	-0.0003 ± 0.0036
Birth weight (n = 221, kg)	-	-	0.0002 ± 0.0005
Weaning weight at 42 d (n = 221, kg)	-	-	0.0051 ± 0.0031
Litter birth weight (n = 2,242, kg)	-	-	0.0002 ± 0.0005
Litter weaning weight at 42 d (n = 2,111, kg)	0.22	0.17	0.0345 ± 0.0557
Backfat thickness (n = 331, mm)	0.20	-0.84	-0.0276 ± 0.0133
Longissimus muscle area (n = 331, cm^2)	0.80	0.20	0.0103 ± 0.0098

Realized heritability estimate of index was 0.19. None of the realized genetic correlations between the index and traits were significant, but the index was highly correlated with backfat. Regression coefficients of mean differences between lines also were not significant. They concluded index selection for post-weaning ADG and BF may decrease backfat and decrease litter size, litter weight and carcass traits slightly.

Summary:

Simulation studies of selection to increase litter size have shown that direct selection for litter size increased litter size more than direct selection for ovulation rate, uterine capacity or embryo survival. Indexes of ovulation rate and uterine capacity, of ovulation rate and embryo survival and of ovulation rate and litter size all increased litter size more than direct selection. Index selection for small placental size

and high placental efficiency is unlikely to increase litter size.

Experimental studies have shown, however, that direct selection for litter size can increase litter size without changing mortality, birth weight and other reproductive traits, but is excepted to increase backfat and decrease growth rate. Index selection for birth weight, placental weight and litter size would be expected to increase litter size. Direct selection for ovulation rate can increase ovulation rate and litter size when ovulation rate is less than dam's uterine capacity. Embryo survival and fetus survival would decrease after 30d of gestation when ovulation rate was greater than dam's uterine capacity. Uterine overcrowding affects embryo and fetus survival when number of fetuses is greater than uterine capacity and will increase number of stillborn pigs and number of mummified pigs. Prenatal survival, embryo and fetus survival, and ovulation rate control the number of pigs born alive at different periods of gestation. Uterine capacity, not ovulation rate, limits litter size in many populations. Direct selection for uterine capacity (litter size) or selection with an index of ovulation rate and prenatal survival would be expected to increase litter size. However, increasing litter size would be expected to cause lighter piglet birth weight and survival to weaning. Moreover, it may result in lighter weaning weights and an increase in piglet mortality from birth to weaning. Selection for maternal farrowing survival can decrease number of stillborn pigs without changing total litter size. Thus, selection with an index of ovulation rate, uterine capacity, birth weight and maternal

farrowing survival may effectively increase sow productivity.

Direct selection for increased growth rate would be expected to increase growth rate and backfat depth. Direct selection for decreased backfat would be expected to decrease backfat depth and reduce growth rate. An index of increased growth rate and decreased backfat with appropriate economic value would be expected to cause greater economic response than direct selection for growth rate or for backfat depth. Direct or index selection for growth, carcass traits and pre-breeding traits only would be expected to have little effect on most reproductive traits, birth weight and weaning weight. Depending on economic values assigned to growth rate and backfat depth, age of puberty could be affected by index selection for growth rate and backfat depth. Long-term selection, however, for growth rate and carcass traits may decrease litter size and decrease piglet survival to birth.

Previous studies have shown the results of index selection for ovulation rate and embryo survival at 50 d of gestation at first 11 generations, continue direct selection three generations for number of fully formed pigs and then direct selection five generations for number of pigs born alive and birth weight in selection line 2; two-stages selection for ovulation rate and litter size for eight generations and continue selection three generations for number of pigs born alive and birth weight in selection line 4, which was derived from the selection line 2 at generation 8, and in selection line 5, which was derived from a control line 1. The selection line 2 and 45,

which was crossed from the selection lines 4 and 5, were selected for increased number of pigs born alive, increased growth rate, decreased backfat, and increased longissimus muscle at the last ten generations, which haven't be studied. Whether number of pigs born still increase after long-term selection? Whether selection for litter size traits and productive traits affects their responses which is not known yet? Genetic and phenotypic responses, genetic and phenotypic correlations and inbreeding effects for all traits will be reported in this study.

Chapter 3

Materials and Methods

Data:

Data were collected from 1981 through 2009 at the University of Nebraska Agricultural and Research Development Center Swine Research Farm. The pedigree file contained 61,081 animals from selection and control lines of a Large White/Landrace composite population beginning with parents of litters born in 1979. Records analyzed were litters of sows farrowing from 1981 when selection was initiated and included number of pigs born alive (BA, n = 5,403), number of fully formed pigs (FF, n = 5,403), number of stillborn pigs (SB, n = 5,403), number of mummified pigs (MUM, n = 5,403), ovulation rate (OR, n = 3,298), number of embryos at 50 d of gestation (ES, n = 1,883), embryo survival rate as a percentage of ovulation rate (SV, n = 1,883), age of puberty (AP, n = 4,842), number of pigs weaned (NW, n = 5,272), litter birth weight (LBW, n = 5,396), litter weaning weight (LWW, n = 5,131), individual birth weight (BW, n = 54,174), individual weaning weight (WW, n = 43,077), individual final weight at about 180 d of age (WT, n = 13,714), individual backfat at age of final weight (BF, n = 5,796), individual average backfat at age of final weight (ABF, n = 7,683) and individual longissimus muscle area at age of final weight (LMA, n = 5,796).

Population and Lines:

This Large White/Landrace composite population was created from 11 Large White and 10 Landrace boars and 40 Large White and 14 Landrace sows. The Large White and Landrace parents were reciprocally mated to produce the F_1 generation of 54 litters. One boar was randomly selected from each F_1 half-sib family and one gilt was randomly selected from each F_1 litter. Those boars and gilts were randomly mated but with full-sib and half-sib matings avoided to produce the F_2 generation of 42 litters. Two boars were randomly selected from each F_2 half-sib family and randomly assigned to either a control line (L1) or a selection line (L2). Approximately two-thirds of the gilts were randomly selected from each F_2 litter and randomly assigned to either L1 or L2. Those boars and gilts were randomly mated but with full-sib and half-sib matings avoided to produce the F_3 generation. The F_3 progeny were designated to be Generation 0.

Descriptions of selected and control lines by generation are given in Figure 1. Over generations there were four selection (Lines 2, 4, 5 and 45) and four control lines (Lines 1, 6, 16 and 61). All lines were derived from the composite population formed be crossing Large White and Landrace in 1979. The F_3 pigs were randomly mated and pigs within litters were assigned to an index line or a control line in 1981 (generation 0, G0). The control line (Line 1) was randomly mated for generations 0 - 23 (a generation interval was one year). The index line (Line 2) was selected for ovulation rate and embryonic survival in generations 0 - 11. Index selection in Line 2 was terminated in Generation 11. For generations 12 - 14, Line 2 was selected for

increased number of fully formed pigs per litter. For generations 15 - 19, Line 2 was selected for increased number of born live pigs per litter and increased birth weight. For generations 20 - 28, Line 2 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area.

At generation 8, Line 2 was used to create selection Line 4 and Line 1 was used to create selection Line 5 and contemporary control Line 6. Parents were re-mated within line after females produced their first litter. This produced a second contemporary group selection and control lines that farrowed six months later than Lines 1 and 2. Line 4 was derived from pigs born to second parity, Line 2 sows. Lines 5 and 6 were derived from pigs born to second parity, Line 1 sows. Line 6 was a control line for Line 4 and Line 5. Lines 4 and 5 were selected in two stages for increased ovulation rate and litter size (uterine capacity) until generation 16. Lines 4 and 5 were selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19 and then crossed to form selection Line 45. Line 45 was selected for increased litter size, increased growth rate, decreased backfat, and increased longissimus muscle area in generations 21- 28. Line 1 and Line 6 were reciprocally crossed in generation 21 to form Line 16 (Line 6 males x Line 1 females), a control line for Line 2, and Line 61 (Line 1 males x Line 6 females), a control line for Line 45.

At generation 18, females of Lines 1 and 2 were inseminated with semen of an

industry maternal line to produce crossbred females for an evaluation of selection response. Pigs in litters by Line 1 females were designated Line 18 and those in litters by Line 2 females were designated Line 28. Line 18 and 28 females were retained as breeders and inseminated with semen of an industry terminal sire line to produce 3-way cross progeny. Reproductive data for the Line 1 and Line 2 females producing these litters and for the Line 18 and Line 28 females were retained as breeders and were included in the database. Results of that experiment were discussed by Petry and Johnson (2004) and Petry et al. (2004) and will not be discussed in this thesis.

At the beginning of the experiment there was an additional selection line (Line 7, selected for increased testis size). Line 7 was subsequently terminated, but pigs of the base generation (n = 154) assigned to it were merged into Line 1 data and are included in this analysis.

Traits Measured, Selection Criteria and Mating:

Selection and control lines were maintained with approximately 40 to 60 litters by 15 to 20 sires per generation. Full-sib and half-sib matings were avoided throughout all generations in all lines.

In control Lines 1, 6, 16 and 61, two sons per sire and one or two gilts per litter were randomly selected each generation: approximately 30 boars and 55 gilts per generation. Two boars (a primary breeder and an alternate breeder) were randomly selected from each paternal half-sib family. One gilt was randomly selected from each

litter and another gilt was selected from randomly selected litters until 55 gilts were selected.

Ovulation Rate and Embryo Survival

Corpora lutea and fetuses (F) were counted via laparotomy of pregnant gilts at 50 days of gestation. Number of corpora lutea was used as a measure of ovulation rate (OR). The ratio of number of fetuses to number of corpora lutea was used as a measure of embryo survived (ES = F/OR).

In control Line 1, laparotomy of pregnant gilts was not practiced in generation 0 (mean of Line 2 recorded in generation 0 was used to represent both Lines 1 and 2); laparomoty was practiced in all Line 1 pregnant gilts during Generations 1-4 and 6-9, but in only one-half of them in Generations 5 and 10.

In selection Line 2, laparotomy was performed in all pregnant gilts during Generations 0-10. Approximately 33% of the highest-ranking gilts were selected on an index of ovulation rate and embryo survived. At birth, two sons of each of the 15 highest ranking dams for the index of ovulation rate and embryo survival calculated from laparotomy data were selected. One was designated a breeder, the other an alternate. In some generations, boars were selected from litters of the 20 highest ranking dams to produce adequate numbers of boars to mate with the selected females. In selection Line 2, selected dams of generation 10 produced the gilts of Generation 11. The gilts from Generation 11 were randomly chosen and laparotomy in them was

not practiced. But sires and gilts of Generation 11 were selected on their dam's index. Thus, 11 generations of index selection were practiced.

The selection index was calculated by traditional selection index methods (Smith, 1967), with the exception that index weights were not economic values but those that maximized expected response in litter size at birth (Johnson et al., 1984). After five generations, it was determined that the index placed too much emphasis on ovulation rate (ovulation rate was increasing rapidly without the expected change in litter size). Thus, the selection index was revised to place more emphasis on embryonic survival and six additional generations of selection were practiced (Neal et al., 1989). The selection index was $I = 10.6 \times OR + 72.6 \times ES$ for Generations 0-5 and $I = 9.9 \times OR + 148.6 \times ES$ for Generations 6-11.

Litter Size (total number of pigs born): Fully Formed Pigs (the sum of live pigs and stillborn Pigs) and Mummified Pigs

Most litters were processed within 2 to 4 hours of completion of parturition. However, litters of sows that began parturition in late afternoon were not processed until the next morning. Thus, all litters were processed within 12 hours of completion of parturition. At processing, numbers of live, stillborn, and mummified pigs were recorded. A pig was classified as stillborn if it was found behind the sow and there was no evidence that it had moved. Mummified pigs were those that were partially decomposed at birth and had obviously died in-utero. Number of fully formed pigs

included the number of pigs born alive and number of stillborn pigs. Number of pigs born alive was defined as the number alive at processing and those deemed to have been alive based on their position and status in the farrowing area.

For Generations 12- 14 in selection Line 2, gilts and boars were selected based on number of fully formed pigs. Two boars (a primary breeder and an alternate breeder) were randomly selected from each of the 15 largest litters. The desired number of gilts was selected from the largest litters, approximately 30%.

For Generations 15-19 in selection Line 2, gilts and boars were selected on number of pigs born alive at the first step. Because the first 14 generations of selection reduced birth weight and postnatal survival rate, gilts and boars selected from the first step were selected for birth weight at the second step. Two boars with heaviest birth weight were selected from each of the 15 largest litters. The desired number of gilts with heaviest birth weight was selected from approximately 50% of largest litters but a maximum of four gilts was selected from a litter.

Weight at 180 d of Age, Backfat Depth and Longissimus Muscle Area

Pigs were weighed to obtain final body weight (kg) and simultaneously scanned for backfat depth (cm) and longissimus muscle area (cm^2) at approximately 180 days of age. Weight was measured by using electronic platform scales. Backfat depth and longissimus area were scanned with an Aloka 500V real-time ultrasound instrument equipped with a 3.5-MHz, 17 cm linear transducer (Corometrics Medical

System, Inc., Wallingford, CT). The probe was placed on the skin approximately 6.4 cm off the midline approximately at the 10^{th} rib. Pigs in the same pen were measured, scanned and recorded on the same day. Pigs within each contemporary group (season-generation) were measured by the same technician and equipment. Pigs within the same contemporary group were usually measured within 2 or 3 days of the same age.

For Generations 20-28 in selection Line 2, gilts and boars were selected on number of pigs born alive and within litter selection for increased growth rate, decreased backfat depth and increased longissimus muscle area. Pigs from approximately 20% of litters with the largest number of pigs born alive were ranked within litter for final weight, backfat depth and longissimus muscle area. The boars and gilts were selected based on 180-d weight, backfat depth and longissimus muscle area. The 15 highest ranking boars, with the restriction that no more than two per litter be selected, were selected as breeders and an additional 5 boars were retained as alternate breeders if a breeder boar died or was injured. The alternates could have been littermates to primary boars and were used as breeders if a primary boar died or failed to breed. As a result, there were four cases during generations 20-28 in which three littermate boars were used as breeders, and one case in which four littermates sired progeny. The highest-ranking gilts were selected from each litter and additional one of second highest-ranking gilts were selected. This resulted in cases where as many as 6 gilts from a litter were selected, although there usually were no more than

three gilts selected per litter.

Two- Stage Selection for Ovulation Rate and Litter Size

At Generation 8, parents of Lines 1 and 2 were re-mated after producing their first litter to produce their second litter. The second litters of Line 2 were used to form Line 4. The second litters of Line 1 were used to form Lines 5 and 6.

For Generations 8-16 in stage 1, all gilts in Lines 4 and 5 from the largest 50% of litters were selected (each line had approximately 100 selected gilts). At stage 2, laparotomy was performed in these gilts after they had expressed their second estrus (the first estrus after pubertal estrus) to count number of corpora lutea as a measure of ovulation rate. These gilts were ranked for ovulation rate and the upper 50% were mated to produce litters. Thus, in gilts, there was a 50% selection rate for litter size in stage 1 and a 50% selection rate for ovulation rate in stage 2. For Generations 8-16 in each of Lines 4 and 5, two boars (a primary breeder and an alternate breeder) were selected from each of the 15 largest litters. Their dams had been selected for ovulation rate so no additional consideration of dam's ovulation rate was given in boar selection. These boars were mated with the gilts that were subsequently selected for ovulation rate to produce the next generation.

For Generations 17-19, Lines 4 and 5 were selected for increased number of pigs born alive and increased birth weight which was the same selection strategy as for Line 2 of Generations 15-19.

At Generation 20, males and females of Lines 4 and 5 were reciprocally crossed to produce Line 45. Because of a policy of limited movement of pigs to control a disease outbreak, no traits other than the litter traits were measured for Lines 4, 5 and 45 at Generation 20.

For Generations 21-28, Line 45 was selected for increased litter size, increased growth rate, decreased backfat, and increased longissimus muscle which was the same selection strategy as for Line 2 of Generations 20- 28.

In Generation 20, Line 2 and Line 4 crossed to form selection Line 24. For Generations 21-26, Line 24 was selected for increased litter size, increased growth rate, decreased backfat, and increased longissimus muscle which was the same selection strategy as for Line 2 of Generations 20- 28. Data from L24 (n =2,598, G21-26) were merged with L2 because selection responses in L24 and L2 were similar.

Management:

Pigs farrowed in summer (Lines 1, 2, 16 24, 18 and 28) of each year will be called summer groups. Pigs farrowed in winter (Lines 4, 5, 6, 45 and 61) of each year will be called winter groups. Pigs with born up to and including on which summer of 1999 and winter of 2000 (Generation 18) for which postweaning traits were recorded and were raised in long modified open-front buildings (MOF) that were naturally ventilated with power curtains controlling airflow. There were 25 pens in each MOF.

Pigs in Generations 19-28 were raised in a confinement building that was mechanically ventilated, heated and cooled. Depending on the season, temperature of the confinement building was between 18.3℃ and 26.7℃. The area for each pen was 8.20 m^2 (1.68 m by 4.88 m) in both buildings.

Weight of all fully formed pigs was recorded at birth. Birth weights of pigs in the same litter were summed and recorded as litter birth weight. Pigs were transferred among litters within and across lines within 1 day after birth in an attempt to create nursing cohorts of 8 ~ 12 piglets. This management practice could be implemented only if matched pairs or sets of sows farrowing within a two-day interval were available. As a result, many nursing litters contained fewer than 8 (11.5%) or more than 12 pigs (12%). To illustrate the effectiveness of the crossfostering practicem the percentages of litters with less than 8 and more than 12 live pigs per litter were 21.1 and 20%, respectively. Pigs were weaned at approximately 28 days of age for Generations 0-12, at approximately 12 days of age for Generations 13-22 and at approximately 18 days of age for Generations 23-28. Number of pigs weaned, weight of each piglet and weaning age were recorded at weaning. The weights and ages at weaning of pigs that were nursed by the same sow were summed and recorded as litter weaning weight and litter weaning age. Pigs were selected and moved from nurseries to pens at approximately 56 days of age for their growth test. Boars and gilts were assigned to different buildings (MOF), or different rooms in the environmentally controlled sapce. Pigs were assigned to pens by age with approximately 10 pigs per

pen. Final weight, backfat depth and longissimus muscle area were obtained at approximately 180 days of age.

The breeding period was approximately five to six weeks. When the oldest gilts in each pen reached 130 days of age, all gilts in the pen were moved daily to an adjacent building for estrus detection where they were exposed for 15 to 20 minutes to a boar. When a gilt first showed the immobile response to a boar, age of puberty was recorded for that gilt. Gilts were mated at approximately 243 days of age so that generation interval was one year. A skip heat management practice was used for gilts whose pubertal estrus occurred at a later age so that all gilts were mated at their third or later estrus. Gilts were mated each day that they were in estrus. They were in pens during the breeding period and placed in stall for the gestation period.

During generations when laparotomy was performed in pregnant gilts to measure ovulation rate and embryo numbers, it was done as often as three times weekly so that all observations occurred as close as possible to 50 days of gestation. Food, but not water, was with held at least 12 hours before laparotomy. After laparotomy, gilts were in recovery rooms for 2 days and then moved back to their stalls. Gilts were fed approximately 1 kg of diet while in recovery.

Pigs were fed a corn-soybean meal diet with different formulas from weaning period to later periods. Percentage of crude protein (CP) in the diet was 21% from entry into the nursery to approximately 12 kg of body weight, 18.2% to 56 d of age, 16% to approximately 55 kg of body weight and 14% to mating age. Percentage of

crude protein (CP) in the sows' diet was 11.5% during the gestation period and 13.2% during the lactation period. The range of metabolizable energy (ME) in the diet was from 3,180 kcal/kg during gestation period to 3,475 kcal/kg during nursery period.

Pigs were fed ad libitum from nursery period until mating. After pigs were mated, they were given approximately 2.1 to 2.3 kg of diet each day, depending on body condition, until 14 d before parturition when intake was increased to 2.5 kg of per day. Sows eat very little feed on the day they farrowed. After farrowing, they daily allotment of feed was increased over the first three days and thereafter they had ad libitum access to feed until weaned.

Data Description:

Summaries of the data for traits were from the MTDF66 and MTDF13 files from running the MTDFPREP program.

Observed numbers, unadjusted means, standard deviations and ranges for traits are given in Table 1. Unadjusted means, standard deviations and ranges for traits with the covariates of age (day), number of nursing pigs (pig) or final weight (kg) are given in Table 2.

Number of levels for fixed effects (contemporary group and sex) and uncorrelated random effects (litter effects and pen-mates effects) are given in Table 3. The numbers of pigs with pen records for final weight, backfat and longissimus muscle area were 6081, 5515, 5516 pigs, respectively.

Number of sires with litter records by line for each generation are given in Table 4. Number of dams with litter records by line for each generation are given in Table 5.

Means, standard deviations and ranges for inbreeding coefficients by line and the average inbreeding coefficients by line for each generation are given in Table 6. As expected, the average inbreeding coefficients became greater as the generation number increased.

Average individual weaning age (day) by line for each generation is given in Table 7. Three sets of data for weaning weight were analyzed: set 1 included pigs with weighted weaning weight at approximately 28 d in generations 0-12, set 2 included pigs weaned at approximately 12 d in generations 13-22, and set 3 included pigs weaned at approximately 18 d in generations 23-28.

Average litter weaning age (day) by line for each generation is given in Table 8.

Statistical Analyses:

MTDFREML (Boldman *et al.*, 1995) was used to obtain estimates of genetic parameters, EBVs and direct and correlated responses. The MTDFNRM program was used for computing the inverse of the additive relationship matrix (A^{-1}) for all animals in the pedigree. The MTDFPREP program was used to calculate coefficients of the relationship matrix for the mixed model equations.

Statistical Models and Mixed Model Equations:

The fixed and random effects in statistical models used to obtain REML estimates of (co)variance components and genetic parameters for each trait are given in Table 9. Depending on the trait, the mixed model included fixed effects of contemporary group and sex with covariates for age, number of nursing pigs or final weight and direct additive genetic, maternal genetic, litter, pen-mates and residual random effects. As shown in Table 9, the mixed models for BW, WW, WT, ABF, BF and LMA included fixed effect of sex. The mixed models for WW, LWW, NW and WT included a fixed covariate of age. The mixed models for LWW and NW included a fixed covariate of number of nursing pigs. The mixed models for ABF, BF and LMA included a fixed covariate of age or a fixed covariate of final weight. Random maternal genetic effects were included in the mixed models for BW, WW, WT and LMA with a fixed covariate of final weight. Independent random pen-mates effects were included in the mixed models for WT, ABF, BF and LMA. Fixed effects of contemporary group and direct additive genetic, litter and residual random effects were included in all mixed models. The equation for the most complete mixed model was:

$$y_{ijklmn} = ctg_m + sex_n + b_1\, age_i + b_2\, nns_i + b_3\, wt_i + a_i + m_j + lit_k + pen_l + e_{ijklmn}$$

where:

y_{ijklmn} is the record of the i^{th} pig at age i with number of nursing mates (nns) i in the l^{th} litter group, the l^{th} pen group, and the m^{th} contemporary group and the n^{th} sex class;

age_i is the covariate for age with linear or quadratic regression coefficient, b_1;

nns_i is the covariate for the number of nursing pigs with quadratic regression coefficient, b_2;

wt_i is the covariate for final weight with linear regression coefficient, b_3;

a_i is the direct additive genetic effect of the i^{th} pig;

m_j is the maternal genetic effect of the dam of the i^{th};

lit_k is the independent random litter effect of the k^{th} litter;

pen_l is the independent random pen-mates effect of the l^{th} pen; and

e_{ijklmn} is the independent random residual effect.

Single-trait models

In matrix notation, the general mixed model for a single trait is:

$$y = X\beta + Z_a a + Z_m m + Z_{lit} lit + Z_{pen} pen + e$$

where:

y is the N × 1 vector of observations;

β is the vector of fixed effects (contemporary group, sex for BW, WW, WT, ABF, BF and LMA with linear regression coefficients for a covariate of

age for WT, and with quadratic regression coefficients for a covariate of age for WW, LWW and NW, and linear regression coefficients for a covariate of age or final weight for BF, ABF and LMA, and quadratic regression coefficient for a covariate of NNS for LWW and NW);

a is the vector of direct additive genetic effects;

m is the vector of maternal genetic effects for BW, WW, WT and LMA with a fixed covariate of final weight;

lit is the vector of independent random litter effects;

pen is the vector of independent random pen-mates effects for WT, ABF, BF and LMA;

e is the vector of independent random residual effects; and

X, Z_a, Z_m, Z_{lit} and Z_{pen} are known incidence matrices relating observations to β, a, m, lit and pen (a, m, Z_a and Z_m are augmented for animals without records that are in the pedigree file).

The expectation of y is:

$E〔y〕 = X\beta$

The expectations of a, m, lit, pen and e are:

$$E\begin{bmatrix} a \\ m \\ lit \\ pen \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

The (co)variance matrix for random effects is:

$$Var\begin{bmatrix} a \\ m \\ lit \\ pen \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 & 0 \\ 0 & 0 & I\sigma_{lit}^2 & 0 & 0 \\ 0 & 0 & 0 & I\sigma_{pen}^2 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

where:

σ_a^2 is the direct additive genetic variance;

σ_m^2 is the maternal genetic variance;

σ_{am} is covariance between direct and maternal genetic effects;

σ_{lit}^2 is the variance due to independent random litter effects;

σ_{pen}^2 is the variance due to independent random pen-mates effects;

σ_e^2 is the variance due to independent random residual effects;

A is the augmented numerator relationship matrix including all animals in the pedigree file; and

the I are identity matrices of appropriate order (number of litters for σ_{lit}^2, number of pen-mates for σ_{pen}^2, and number of records for σ_e^2).

<u>Two-trait models</u>

The symbols in matrix notation for two trait model are the same as the description for a single trait.

The expectation of y is:

E〔y〕= Xβ

The expectations of trait i of a_i, m_i, lit_i, pen_i and e_i, i = 1 or 2 are:

$$E\begin{bmatrix} a_i \\ m_i \\ lit_i \\ pen_i \\ e_i \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

The (co)variance matrix for mixed model is:

$$Var\begin{bmatrix} a_1 \\ m_1 \\ a_2 \\ m_2 \\ lit_1 \\ pen_1 \\ lit_2 \\ pen_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A\sigma^2_{a_1} & A\sigma_{a_1m_1} & A\sigma_{a_1a_2} & A\sigma_{a_1m_2} & 0 & 0 & 0 & 0 & 0 & 0 \\ A\sigma_{a_1m_1} & A\sigma^2_{m_1} & A\sigma_{a_2m_1} & A\sigma_{m_1m_2} & 0 & 0 & 0 & 0 & 0 & 0 \\ A\sigma_{a_1a_2} & A\sigma_{a_2m1} & A\sigma^2_{a_2} & A\sigma_{a_2m_2} & 0 & 0 & 0 & 0 & 0 & 0 \\ A\sigma_{a_1m_2} & A\sigma_{m_1m_2} & A\sigma_{a_2m_2} & A\sigma^2_{m_2} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & I\sigma^2_{lit_1} & 0 & I\sigma_{lit_1lit_2} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & I\sigma^2_{pen_1} & 0 & I\sigma_{pen_1pen_2} & 0 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_{lit_1lit_2} & 0 & I\sigma^2_{lit_1} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & I\sigma_{pen_1pen_2} & 0 & I\sigma^2_{pen_2} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & I\sigma^2_{e_1} & I\sigma_{e_1e_2} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & I\sigma_{e_1e_2} & I\sigma^2_{e_2} \end{bmatrix}$$

where:

$\sigma^2_{a_i}$ is the direct additive genetic variance for trait i, i = 1or 2;

$\sigma^2_{m_i}$ is the maternal genetic variance for trait i, i = 1or 2;

$\sigma_{a_ia_j}$ is the covariance between direct genetic effect for trait i and direct genetic effect for trait j, i = 1 and j = 2;

$\sigma_{a_im_j}$ is the covariance between direct genetic effect for trait i and maternal genetic effect for trait j, i = 1 and j = 2;

$\sigma_{m_im_j}$ is the covariance between maternal genetic effect for trait i and maternal genetic effect for trait j, i = 1 and j = 2;

$\sigma^2_{lit_i}$ is the variance due to independent random litter effects for trait i, i = 1 or 2;

$\sigma^2_{pen_i}$ is the variance due to independent random pen-mates effects for trait i, i = 1 or 2;

$\sigma_{lit_i lit_j}$ is the covariance between random litter effects for trait i and random litter effects for trait j, i = 1 and j = 2;

$\sigma_{pen_i pen_j}$ is the covariance between random pen-mates effects of trait i and random pen-mates effects of trait j, i = 1 and j = 2;

$\sigma^2_{e_i}$ is the variance due to independent random residual effects for trait i, i = 1 or 2;

$\sigma_{e_i e_j}$ is the covariance between random residual effects for trait i and random residual effects for trait j, i = 1 and j = 2;

A is the augmented numerator relationship matrix including all animals in the pedigree file; and

the I are identity matrices of appropriate order (number of litters for $\sigma^2_{lit_i}$, number of pen-mates for $\sigma^2_{pen_i}$, number of records for $\sigma^2_{e_i}$, number of litters for trait i and trait j for $\sigma_{lit_i lit_j}$, number of pen-mates for trait i and trait j for $\sigma_{pen_i pen_j}$ and number of records for trait i and trait j for $\sigma_{e_i e_j}$, i = 1 and j = 2).

Starting values for variance components were required to run MTDFRUN

program, which was used to obtain estimates of variance components. From the unadjusted standard deviations shown in Table 1, phenotypic variance of each trait was used to calculate starting values for variance components for direct genetic, maternal genetic, litter, pen-mates and residual effects and direct-maternal genetic covariance. The sum of starting values for variance components should often be about or usually less than 2/3 of the unadjusted phenotypic variance (L. D. Van Vleck personal communication, 2005). For each trait, two-thirds of the unadjusted phenotypic variance was multiplied by assumed heritability (0.5 for WT, BF and ABF; about 0.7 for LMA and about 0.15 for other traits) to obtain starting values for direct additive genetic variance (σ_a^2) and was multiplied by 0.1 to obtain starting values for maternal genetic variance (σ_m^2) for BW, WW and WT. Starting values for direct-maternal genetic covariance for BW, WW and WT were estimated from starting values of direct additive genetic variances and maternal genetic variances and reasonable correlation coefficients. Reasonable starting values were guessed at litter, pen-mates and residual effects. When starting values have a large difference from globally converged estimates of variance components, the final converged estimates of variance components may not be real estimates of variance components. For more precise estimates, two or several sets of different starting values were used and estimates were assumed to be best estimates of population parameters if the same estimates of variance components and/or logarithm of the likelihood for the model of each trait were obtained. The convergence criterion was set at 1×10^{-6} for the variance

of -2 the logarithms of the likelihood (-2 logL) in the simplex. The number of simplex rounds was set to 500 rounds for models without maternal genetic effects and pen-mates effects. The number of simplex rounds was set to 800 ~ 3500 rounds for other models. After the convergence criterion was obtained, several additional restarts were executed until –2 logL did not change at the third decimal. The time and number of restarts were less if the starting values were similar to estimates of the final convergence. If there is confounding of effects that prevents separation of some variance components, unique final convergence may not be reached or estimates of variance components from several sets of different starting values may not be the same. Restarts were ended when estimates of variance components were similar or the same for the last three restarts.

Test of significance of linear and/or quadratic regression coefficients for covariates of age and number of pigs nursed and inbreeding coefficients for traits are given in Table 10. The linear effect of age was significant for litter weaning weight at 28 d, 12 d and 18 d, number of pigs weaned at 12 d and weaning weight at 28 d, 12 d and 18 d ($P < 0.01$). The quadratic effect of age was significant for litter weaning weight at 28 d ($P < 0.01$), number of pigs weaned at 28 d ($P < 0.05$) and 12 d ($P < 0.01$) and weaning weight at 28 d ($P < 0.01$) and 18 d ($P < 0.01$). There was a linear effect of number of pigs nursed on litter weaning weight and number of pigs weaned at 28 d, 12 d and 18 d ($P < 0.01$). Although the quadratic regression coefficient for age was not significant for litter weaning weight, number of pigs

weaned and weaning weight at all weaning ages (28, 12 and 18 d), it was for some and to be consistent, the quadratic regression was included in analysis of litter weaning weight at all ages.

A linear effect of age on final weight, backfat depth of 10^{th} rib, average backfat depth and longissimus muscle area existed ($P < 0.01$). and when backfat depth and muscle area were analyzed with weight, but not age in the model, a linear effect of weight existed for backfat depth of 10^{th} rib ($P < 0.05$), average backfat depth ($P < 0.01$) and longissimus muscle area ($P < 0.01$).

The linear effect of inbreeding coefficients existed for number of pigs born alive ($P < 0.01$), number of embryos survived ($P < 0.01$), embryo survival rate ($P < 0.05$), age of puberty ($P < 0.01$), number of fully formed pigs ($P < 0.01$), number of mummified pigs ($P < 0.05$), litter birth weight ($P < 0.01$), individual birth weight ($P < 0.05$), final weight at 180 d of age ($P < 0.01$), backfat depth of 10^{th} rib adjusted for age ($P < 0.05$), average backfat depth adjusted for age ($P < 0.05$) and longissimus muscle area adjusted for age ($P < 0.01$). The covariate of inbreeding coefficients was not included in models of all traits because the inbreeding coefficients were not included in selection criteria in this experiment and estimates of variance components for models without a covariate of inbreeding coefficients were similar to models with a covariate of inbreeding coefficients. Only results for models not including a covariate of inbreeding coefficients are reported for all traits.

Comparison of -2 logL at convergence for the model with maternal genetic

effects and without maternal genetic effects and tests of significance of differences in –2 logL between the model with maternal genetic effects and without maternal genetic effects are given in Table 11. The chi-square test provides evidence that there is a statistically significant difference between models with maternal genetic effects and models without maternal genetic effects for birth weight, weaning weight at 28 d and at 12 d and final weight ($P < 0.01$, $X^2_{2, 0.01} = 9.210$). The results indicate that maternal genetic effects should be included in the models for birth weight, weaning weight for all data sets and final weight, although the chi-square test for weaning weight at 18d was not significant. The chi-square test for longissimus muscle area approached significant ($P < 0.05$, $X^2_{2, 0.05} = 5.991$). Thus, maternal effects were included in the model of longissimus muscle area.

Estimates of variance components for models of backfat depth of 10^{th} rib and average backfat depth without maternal genetic effects were similar to models with maternal genetic effects. Only results for models not including maternal genetic effects are reported for backfat depth of 10^{th} rib and average backfat depth.

Estrus number at conception was not included in the models in this study because only a few gilts were mated at first and second estrus.

Day of gestation when laparotomy was performed was not included in the models of embryo number and embryo survival because most pregnant gilts were laparotomized at 49, 50 or 51 days of gestation.

The MTDFREML program with OPTION 4 and with final estimates of

variance components was used to obtain means of EBVs and phenotypes by generation for each line for animals with records. A fixed factor of line × generation was added to the original model of all traits. SAS (1996) program with GLM procedure was used to compute and plot genetic trends and phenotypic trends by linear and quadratic regression of mean EBVs and phenotypes on generation for each line. L1, L6, L16 and L61 had similar phenotypic and genetic trends and were averaged to illustrate responses in control lines (LC).

Realized Selection Differentials and Cumulative Selection Differentials:

Traits measured on only female:

The realized selection differential of "male" in generation n (S_n^m) was the average differential between phenotypic line-generation mean of generation n and phenotypic mean of selected dams born in generation n weighted by the number of their grand-daughters through sons measured in generation n+2. The formulation of selection differential was:

$$S_n^m = \frac{1}{\sum D_k} \sum_{k=1}^{k} \left[(P_{n_k} - \bar{P}_n) \times D_k \right] \qquad n \geq 0, k \geq 1$$

where:

S_n^m is the selection differential of "male" in generation n, n = 0, 1, …, n;

P_{n_k} is the phenotypic mean of the k[th] selected dam born in generation n having grand-daughters through sons measured in generation n+2, n = 0, 1, …, n, k = 1, 2, …, k;

$\bar{P}_n$ is the phenotypic mean of generation n, n = 0, 1, …, n;

D_k is the number of grand-daughter through sons measured in generation n+2 of selected dam k, n = 0, 1, …, n, k = 1, 2, …, k;

The realized selection differential of females in generation n (S_n^f) was the average differential between phenotypic line-generation mean of generation n and phenotypic mean of selected dams born in generation n weighted by the number of their daughters measured in generation n+1. The formulation of selection differential was:

$$S_n^f = \frac{1}{\sum D_k} \sum_{k=1}^{k} \left[(P_{n_k} - \bar{P}_n) \times D_k \right] \qquad n \geq 0, k \geq 1$$

where:

S_n^f is the selection differential of females in generation n, n = 0, 1, …, n;

P_{n_k} is the phenotypic mean of the k[th] selected dams born in generation n having daughters measured in generation n+1, n = 0, 1, …, n, k = 1, 2, …, k;

$\bar{P}_n$ is the phenotypic mean of generation n, n = 0, 1, …, n;

D_k is the number of daughters measured in generation n+1 of selected dam k, n = 0, 1, …, n, k = 1, 2, …, k;

The realized cumulative selection differential for OR, ES, SV, FF or BA was:

CSD_0(OR, ES, SV, FF, BA) = 0

CSD_1(OR, ES, SV, FF, BA) = $\frac{1}{2} S_0^f$

CSD_n(OR, ES, SV, FF, BA) = $\frac{1}{2} S_{n-1}^f + \frac{1}{4} \sum_{i=0}^{n-2} (S_i^m + S_i^f) \quad n \geq 2, n-2 \geq i \geq 0$

where:

CSD_0 is the cumulative selection differential on measured females of generation 0;

CSD_1 is the cumulative selection differential on measured females of generation 1;

CSD_n is the cumulative selection differential on measured females of generation n, n = 2, …, n;

S_0^f is the selection differential of female in generation 0;

S_{n-1}^f is the selection differential of female in generation n-1, n = 2, …, n;

S_i^m is the selection differential of “male” in generation i, i = 0, 1, …, n-2;

S_i^f is the selection differential of female in generation i, i = 0, 1, …, n-2.

Traits measured on both sexes:

The realized selection differential of male or female on generation n (S_n^m or S_n^f) was averaged the differential between phenotypic line-generation mean of generation n and phenotypic mean of selected sires or dams born in generation n weighted by the number of their progeny measured in generation n+1. The formulation of selection differential was:

$$S_n^m \text{ or } S_n^f = \frac{1}{\sum D_k} \sum_{k=1}^{k} \left[(P_{n_k} - \bar{P}_n) \times D_k \right] \qquad n \geq 0, k \geq 1$$

where:

S_n^m is the selection differential of measured males in generation n, n = 0, 1, …, n;

S_n^f is the selection differential of measured females in generation n, n = 0, 1, …, n;

P_{n_k} is the phenotypic mean of selected parent k born in generation n having progeny measured in generation n+1, n = 0, 1, …, n, k = 1, 2, …, k;

$\bar{P}_n$ is the phenotypic mean of generation n, n = 0, 1, …, n;

D_k is the number of progeny measured in generation n+1 of selected parent k, n = 0, 1, …, n, k = 1, 2, …, k;

The realized cumulative selection differential for BW, WT, BF or LMA was:

CSD_0(BW, WT, BF, LMA) = 0

CSD_n(BW, WT, BF, LMA) = $\frac{1}{2}\sum_{i=0}^{n-1}(S_i^m + S_i^f)$ $\quad n \geq 1, n-1 \geq i \geq 0$

where:

CSD_0 is the cumulative selection differential on measured pigs of generation 0;

CSD_n is the cumulative selection differential on measured pigs of generation n,

n = 1, …, n;

S_i^m is the selection differential of male in i, i = 0, 1, …, n-1;

S_i^f is the selection differential of female in generation i, i = 0, 1, …, n-1.

Chapter 4

Results

Realized Cumulative Selection Differentials for Selection Traits:

Realized cumulative selection differentials for selection traits by line and generation are given in Tables 12-17. Trends of cumulative selection differentials on generation for traits by line are given in Figures 2.1 – 2.9.

Ovulation Rate, Embryo Survived and Embryo Survival Rate

Realized cumulative selection differentials at Generation 11 for OR, ES and SV were -0.77 ova, 0.33 embryos and 0.16% in LC, and 24.61 ova, 15.90 embryos and 0.07% in L2. Realized cumulative selection differentials at Generation 16 for OR in LC, L4 and L5 were -0.14, 22.44 and 2.79 ova, respectively. Realized cumulative selection differentials for OR were negative in LC, but positive for all selection lines, except for L5 at G9 and G10. In L5, the increase of cumulative selection differentials at G10 was still less than the decrease of cumulative selection differentials before being derived from LC. When selection was for OR and ES during G 0-11, selection differentials per generation for OR and ES in L2 for G 6-11 (I = 9.9 OR + 148.6 ES) were greater than that for G 0-5 (I = 10.6 OR + 72.6 ES). Selection differentials per generation for SV in L2 for two index periods were similar and positive. When

selected for OR and LS for G 8-16, selection differential per generation for OR in L4 was greater than that in L5. Coefficients for regression of cumulative selection differential on generation for OR, ES and SV by lines were:

	Selection Differentials Per Generation for Traits		
	OR	**ES**	**SV**
LC (Mean)	0.003	0.069	0.018
L2 (G 0-5)	1.829	1.386	0.004
L2 (G 6-11)	2.589	1.585	0.004
L2 (G 0-11)	1.999	1.504	0.007
L4	0.680	~	~
L5	0.450	~	~

Fully Formed Pigs and Pigs Born Alive

Realized cumulative selection differentials for FF and BA were similar in all lines (Tables 13 and 14). When L2 was selected for OR and ES during G 0-11, selection differentials increased 0.425 FF and 0.438 BA per generation. When L2 was direct selected for FF during G 12-14, selection differentials increased 1.637 FF and 1.387 BA per generation. When selected for OR and LS during G 8-16, selection differentials per generation in L4 were somewhat greater for FF and BA than in L5. When selected for BA and BW in L2 (G 15-19), L4 (G 17-19) and L5 (G 17-19), selection differentials per generation in L4 increased more FF and BA than they did in L5 and L2 (L4 > L5 > L2). When selected for BA, WT, BF and LMA in L2 (G 20-27) and L45 (G 20-26), selection differentials per generation in L2 for FF and BA were more than in L45 (L2 > L45). Selection differential in LC increased 0.152 FF and

0.167 BA per generation. Coefficients for regression of cumulative selection differential on generation for FF by lines and selection traits were:

	Selection Differentials Per Generation for Number of Fully Formed Pigs					
	OR+ES	**OR+LS**	**FF**	**BA+BW**	**BA+WT+BF+LMA**	**Mean**
LC	~	~	~	~	~	0.152
L2	0.425	~	1.637	1.226	1.307	0.969
L4	~	1.518	~	1.411	~	1.517
L5	~	1.208	~	1.233	~	1.269
L45	~	~	~	~	1.251	1.251

Coefficients for regression of cumulative selection differential on generation for BA by lines and selection traits were:

	Selection Differentials Per Generation for Number of Pigs Born Alive					
	OR+ES	**OR+LS**	**FF**	**BA+BW**	**BA+WT+BF+LMA**	**Mean**
LC	~	~	~	~	~	0.167
L2	0.438	~	1.387	1.209	1.494	0.985
L4	~	1.301	~	1.574	~	1.425
L5	~	1.115	~	1.502	~	1.275
L45	~	~	~	~	1.364	1.364

Birth Weight

Realized cumulative selection differentials for BW in L2 and L45 were greater than LC during G 20-27 (Table 15). Selection differential per generation for BW was small in all lines. Coefficients for regression of cumulative selection differential on generation for BW by lines and selection traits were:

	Selection Differentials Per Generation for Birth Weight					
	OR+ES	**OR+LS**	**FF**	**BA+BW**	**BA+WT+BF+LMA**	**Mean**
LC	~	~	~	~	~	0.059
L2	0.055	~	0.008	0.051	0.110	0.062
L4	~	0.070	~	0.147	~	0.094
L5	~	0.017	~	0.115	~	0.043
L45	~	~	~	~	0.144	0.144

Weight at 180 d of Age

Realized cumulative selection differential for WT in L45 was 61.17 kg at G 27, which is about 1.8 times the cumulative selection differential in L2 and about 3.8 times the cumulative selection differential in LC (Table 16). Cumulative selection differentials were negative in L4 and in L2 from G 2 to G 22. When L2 was selected for OR and ES during G 0-11, selection differential for WT was negative. When selected for OR and LS for G 8-16, selection differentials per generation for WT in L5 increased more than in L4 (L5 > L4). When selected for BA and BW in L2 (G 15-19), L4 (G 17-19) and L5 (G 17-19), selection differentials per generation in L2 increased more than in L5 and L4 (L2 > L5 > L4). When selected for BA, WT, BF and LMA in L2 (G 20-27) and L45 (G 21-27), selection differentials per generation for WT in L45 increased more than in L2 (L45 > L2). Selection differential for WT in LC were 0.611 kg per generation. Coefficients for regression of cumulative selection differential on generation for WT by lines and selection traits were:

	Selection Differentials Per Generation for Final Weight at 180 d Of Age					
	OR+ES	**OR+LS**	**FF**	**BA+BW**	**BA+WT+BF+LMA**	**Mean**
LC	~	~	~	~	~	0.611
L2	-1.958	~	0.917	1.780	5.453	0.567
L4	~	2.029	~	0.841	~	1.474
L5	~	2.531	~	1.023	~	2.063
L45	~	~	~	~	6.845	6.845

Backfat Depth Of The 10th Rib and Longissimus Muscle Area

Realized cumulative selection differential for BF at G 27 in L45 was greater than in L2, but realized cumulative selection differential for LMA was less (Table 17). Coefficients for regression of cumulative selection differential on generation for BF and LMA by lines and selection traits were:

Selection Differentials Per Generation when selected BA, WT, BF and LMA		
	Backfat Depth Of The 10th Rib	**Longissimus Muscle Area**
LC	0.009	0.071
L2	-0.059	1.698
L45	-0.137	1.648

Estimates of (co)variance components:

REML estimates of phenotypic variance and fractions due to litter, pen-mates and residual effects; direct and maternal heritability, and direct-maternal genetic correlation for traits are given in Table 18. Most reproductive traits had low estimates of direct heritability (0.11 ~ 0.27), except for OR (0.27), AP (0.57), LBW (0.34), all LWW (28 d: 0.21; 12 d: 0.21; 18 d: 0.27) and NW at 18 d of age (0.23). BW and all

WW had very low estimates of direct heritability (0.01 ~ 0.06). WT, BF and LMA at 180 d of age had moderate to high estimates of direct heritability. Estimates of maternal heritability for BW, WW at 28d (G 0-12) and WW at 12 d (G 13-22) were about twice or more than estimates of direct heritability. Estimate of maternal heritability for WW at 18 d (G 23-28) was similar to its estimate of direct heritability. Estimates of maternal heritability for WT at approximate 180 d and LMA adjusted for WT were much smaller than their estimates of direct heritability. SE for all direct and maternal heritability were small (0.02~0.07). There was a low, negative, correlation between direct and maternal genetic effects for WW at 28 d (G 0-12, -0.06), and this correlation for WW at 18d (G 23-28) was zero. However, the correlation between direct and maternal genetic effects for WW at 12 d (G 13-22) was near one (0.98). The correlation between direct and maternal genetic effects for LMA with a covariate of WT was negative (-0.74). Estimates of fractions of phenotypic variance due to litter effects for all reproductive traits, WT and all carcass traits were small (0.00 ~ 0.11), but for BW, WW at 18 d, 12 d and 18 d of age were 0.17, 0.22, 0.23 and 0.24 respectively. Fractions of estimates of phenotypic variance due to residual effects for all traits were 0.41 ~ 0.88.

Genetic and phenotypic correlations between traits:

Genetic and phenotypic correlations between traits are given in Tables 19.1-19.4.

Genetic and phenotypic correlations of pigs born alive with other traits

The genetic correlations of BA with most reproductive traits, except for ES, FF and LBW were low (0.00 ~ ± 0.20) to moderate (± 0.21 ~ ± 0.50). The genetic correlation of BA with ES was 0.49 and the phenotypic correlation was 0.51. The genetic and phenotypic correlations of BA with LBW were quite high (r_g = 0.68 and r_p = 0.76). The genetic and phenotypic correlations (r_g = 0.89 and r_p = 0.84) between BA and FF were very high. The genetic and phenotypic correlations (r_g = 0.30 and r_p = 0.36) between BA and SV were moderate and positive. Selection for BA is expected to increase genetic responses in ES, FF and LBW and may increase genetic responses in SV.

Selection for BA is not expected to produce large genetic responses for BW, WT, BF, ABF and LMA, because all genetic correlations of BA with these traits were small. Selection for BA may increase genetic response in WW at 28 d (G 0-12, r_g = 0.32) and WW at 12 d (G13-22, r_g = 0.46).

Genetic and phenotypic correlations of fully formed pigs with other traits

Because BA and FF had very highly positive genetic and phenotypic correlations, the genetic and phenotypic correlations of FF with other traits were similar to that of BA with other traits. Correlations of FF with ES and LBW were high and positive. However, SB was negatively correlated genetically and phenotypically with BA (r_g = -0.07 and r_p = -0.21) but had positively correlated genetically and

phenotypically with FF (r_g = 0.39 and r_p = 0.35). The genetic correlation of SV with BA was 0.30 but with FF was 0.13. The genetic and phenotypic correlations of NW at 12 d (G 12-21) with BA were similar to FF.

The genetic and phenotypic correlations of FF with BW, WW, WT, BF, ABF and LMA were small (r = -0.13 ~ 0.15), except the genetic correlation of FF with WW at 28 d was moderate (G 0-12, r_g = 0.41); WW at 12 d was more highly correlated with FF (G13-22, r_g = 0.59).

Genetic and phenotypic correlations of ovulation rate with other traits

OR had low to moderate genetic and phenotypic correlations with most reproductive traits, except for genetic correlations with SV (r_g = -0.81) and SB (r_g = 0.53).

Selection for OR is not expected to produce large genetic responses for BW, WW, WT, BF, ABF and LMA, because all genetic correlations of OR with these traits were small (r = -0.16 ~ 0.12).

Genetic and phenotypic correlations of embryo survival with other traits

Selection for ES would not result in large genetic responses for most reproductive traits, except for FF and SB. Selection for ES is expected to increase genetic responses in FF and SB.

Selection for ES is not expected to produce much genetic responses in WW at

28 d (G 0-12), WT and ABF because genetic correlations of ES with them were small (r = -0.16 ~ 0.12). Selection for ES may decrease genetic response in BW because there was a moderate genetic correlation between ES and BW (r_g = -0.23).

Genetic and phenotypic correlations of birth weight with other traits

Selection for BW is expected to increase genetic responses for WW at 12 d (G13-22) and WW at 18 d (G23-28) because of their high positive correlations. Selection for BW may increase genetic responses for WW at 28 d (G 0-12), WT and BF and decrease response in LMA. Selection for BW is not be expected to have large effects on other carcass traits.

Genetic and phenotypic correlations of weight at 180 d of age with other traits

Selection for WT at 180 d of age is expected to increase genetic responses for BF, ABF and LMA. Selection for WT would also increase genetic responses for WW at 28 d (G 0-12), at 12 d (G 13-22) and at 18 d (G 23-28).

Genetic and phenotypic correlations of backfat depth of the 10th rib with other traits

Selection for decrease BF (adjusted for WT) may increase genetic response in LMA because there was a moderate and negative genetic correlation between BF and LMA.

Genetic and phenotypic correlations of longissimus muscle with other traits

Selection for increase LMA (adjusted for WT) is expected to decrease genetic response for WW at 12 d (G 13-22).

Selection for increase LMA (adjusted for age) is expected to increase genetic response for WT ($r_g = 0.53$).

Estimated genetic and phenotypic trends by line:

Coefficients (b) and SE for regression of mean estimated direct and maternal breeding values and phenotypic means on generation for control Line C by trait are given in Tables 20.1 and 20.2. Coefficients and SE for genetic and phenotypic responses were small for all traits in LC.

Coefficients (b) and SE for regression of mean estimated direct and maternal breeding values on generation for selection Lines 2, 4, 5 and 45 by trait are in Tables 21 and 22. Coefficients (b) and SE for regression of phenotypic means on generation are in Tables 23 and 24.

Ovulation Rate, Embryo Survived and Embryo Survival Rate

Estimated genetic trends for ovulation rate and embryo number by line are given in Figures 3 and 4, respectively. Estimated phenotypic trends are in Figures 5 and 6, respectively. Genetic response to index selection for OR and ES in L2 resulted in a linear increase in number of ova of 0.525 ± 0.012 per generation and number of

embryos of 0.258 ± 0.007 per generation ($P < 0.01$). Phenotypic responses were 0.768 ± 0.062 ova and 0.294 ± 0.026 embryos per generation ($P < 0.01$). In L2, both periods of index selection for OR and ES [I(G0-5) = 10.6 OR + 72.6 ES and I(G6-11) = 9.9 OR + 148.6 ES] increased pigs born alive, although the genetic correlations between BA and OR were small (r_a = -0.05). The genetic correlations between BA and ES were positive (r_a = 0.49 and r_p = 0.51) and index weightings on ES were greater than weightings on OR in both periods, which can explain why number of pigs born alive was still increased in both periods when there was a small and negative genetic correlation between BA and OR.

Genetic response to two-stage selection for OR and LS in L4, which was derived from selection line 2 and under was under more intense selection for uterine capacity, resulted in an increase of 0.049 ± 0.031 ova per generation. Genetic response to two-stage selection for OR and LS in L5, which was derived from control line and was, because it was derived from a line with lower OR, was selected more for OR than uterine capacity, resulted in an increase of 0.211 ± 0.015 ova per generation ($P < 0.01$). Phenotypic response to two-stage selection for OR and LS in L4 resulted in less increase in number of ova than in L5. Index selection for OR and ES (L2, G 0-11) increased ovulation rate faster than two-stage selection for OR and LS (L4 and L5, G 8-16).

Estimated genetic and phenotypic trends for embryo survival rate by line are given in Figures 7 and 8, respectively. Selection for OR and ES in L2 from G 0-11

slightly decreased response in SV (b = - 0.002 ± 0.001% per generation, P < 0.01). The phenotypic response in SV was also negative (b = - 0.010 ± 0.002% per generation, P < 0.01). The index used in selection for OR and ES caused a decrease in embryonic survival.

Fully Formed Pigs, Pigs Born Alive, Stillborn Pigs and Mummified pigs

Estimated genetic trends for number of fully formed pigs per litter by line are given in Figure 9. Selection for OR and ES in L2 increased FF 0.119 ± 0.008 pigs per generation (P < 0.01). Two-stage selection for OR and LS in L4 and L5 (L4: 0.265 ± 0.012 pigs/generation and L5: 0.292 ± 0.011 pigs/generation, G 8-16, P < 0.0001) increased FF more rapidly than direct selection for FF in L2 (0.195 ± 0.017 pigs/generation, G 12-14, P < 0.1). This result is in agreement with Bennett and Leymaster (1990). When selection was for BA and BW, correlated responses in FF in L5 were larger than that in L2 and L4, and correlated responses in FF in L2 and L4 were similar (L2: 0.120 ± 0.033 pigs/generation, G 15-19, P < 0.05; L4: 0.110 ± 0.019 pigs/generation, G 8-16; L5: 0.464 ± 0.054 pigs/generation, G 8-16, P < 0.1). When lines were selected for BA, WT, BF and LMA, correlated responses in FF in L2 and L45 were similar (L2: 0.165 ± 0.037 pigs/generation, G 20-27, P < 0.01; L45: 0.171 ± 0.030 pigs/generation, G 20-26, P < 0.01).

Estimated genetic trends for number of pigs born alive per litter by line are given in Figure 10. Selection for OR and ES in L2 increased BA 0.052 ± 0.007 pigs

per generation ($P < 0.01$). Two-stage selection for OR and LS in L5 increased BA more rapidly than that in L4, and direct selection for FF in L2 (L2: 0.222 ± 0.006 pigs/generation, G 12-14, $P < 0.01$; L4: 0.186 ± 0.018 pigs/generation and L5: 0.281 ± 0.011 pigs/generation, G 8-16, $P < 0.01$). Selections for BA and BW in L5 produced responses in BA that were larger than that in L2 and L4 (L2: 0.123 ± 0.025 pigs/generation, G 15-19, $P < 0.05$; L4: 0.168 ± 0.029 pigs/generation, G 17-19; L5: 0.389 ± 0.058 pigs/generation, G 17-19, $P < 0.1$). When selected for BA, WT, BF and LMA, correlated responses in BA in L2 and L45 were similar (L2: 0.176 ± 0.024 pigs/generation, G 20-27, $P < 0.01$; L45: 0.170 ± 0.028 pigs/generation, G 20-26, $P < 0.01$).

Estimated genetic trends for number of stillborn pigs per litter by line are given in Figure 11. Selection for OR and ES in L2 increased SB 0.068 ± 0.004 pigs per generation (G 0-11, $P < 0.01$). When the selection emphasis was on FF (G 12-14), BA and BW (G 15-19) and to BA, WT, BF and LMA (G 20-27), correlated responses in SB in L2 decreased 0.014 ± 0.004 per generation (G 12-27, $P < 0.01$). Two-stage selection for OR and LS in L4 ($P < 0.01$) and L5 ($P < 0.05$) caused a small increase of 0.059 ± 0.015 and 0.011 ± 0.004 SB per generation, respectively. Selection for BA and BW decreased SB 0.038 ± 0.006 pigs per generation in L4 ($P < 0.1$) but increased SB 0.048 ± 0.009 pigs per generation in L5. Selection for BA, WT, BF and LMA in L45 did not affect SB (b = -0.003 ± 0.010 pigs/generation, G 20-26).

Estimated genetic trends for number of mummified pigs per litter by line are

given in Figure 12. Selection for OR and ES in L2 increased MUM 0.048 ± 0.007 pigs per generation before generation 6 (I = 10.6 OR + 72.6 ES, G 0-5, $P < 0.05$) but decreased MUM 0.027 ± 0.006 pigs per generation after generation 6 (I = 9.9 OR + 148.6 ES, G 6-11, $P < 0.05$). The change in index weights to greater emphasis on embryo survival decreased the incidence of mummified piglets. However, the control line C had opposite responses in MUM before (b = -0.053 ± 0.003 pigs/generation, $P < 0.01$) and after (b = 0.038 ± 0.005 pigs/generation, $P < 0.01$) generation 6. Because selection was random, this change was due either to genetic drift or to changes in environmental effects across generations. Selection for FF (G 12-14) and for BA and BW (G 15-19) in L2 decreased MUM 0.03 ± 0.00 and 0.02 ± 0.00 pigs per generation, respectively ($P < 0.05$). Selection for BA, WT, BF and LMA in L2 did not affect MUM. In generations 8-14, MUM in L4 decreased 0.026 ± 0.009 pigs per generation ($P < 0.05$), but in L5 increased MUM 0.037 ± 0.007 pigs per generation ($P < 0.01$). In generation 14-19, correlated responses in MUM in L4 were almost zero (b = 0.0002 ± 0.0035), and in L5 decreased MUM 0.04 ± 0.01 pigs per generation ($P < 0.01$). Therefore, selection for BA resulted in decreased number of MUM. However, MUM increased in L45 during generations 20-27 when selection was for BA, WT, BF and LMA (0.02 ± 0.01 MUM per generation, $P < 0.01$).

Estimated phenotypic trends for number of fully formed and born alive pigs per litter by line are given in Figures 13 and 14, respectively. Phenotypic responses in FF and BA increased in each selection line over 28 generations, except for FF in L4

during generations 8-19. Two-stage selection for OR and LS in L4 resulted in an increase of 0.271 ± 0.083 FF pigs per generation (G 8-16, $P < 0.05$).

Estimated phenotypic trends for number of stillborn pigs per litter by line are given in Figure 15. Phenotypic trends for SB in selection lines were similar to genetic trends. Selection for OR and ES in L2 resulted in phenotypic responses in SB of 0.12 ± 0.02 pigs per generation (G 0-11, $P < 0.01$). Selection for BA and BW in L4 decreased phenotypic responses in SB ($P < 0.5$). Selection for BA, WT, BF and LMA in L45 decreased SB 0.10 ± 0.03 pigs per generation (G 20-26, $P < 0.05$).

Estimated phenotypic trends for number of mummified pigs per litter by line are given in Figure 16. For generations 0-11, the phenotypic trend of control line C was opposite to its genetic trend but was similar to phenotypic trend of L2. Selection for OR and ES in L2 increased MUM 0.28 ± 0.06 pigs per generation before generation 6 (I = 10.6 OR + 72.6 ES, G 0-5, $P < 0.005$) but decreased MUM 0.32 ± 0.05 pigs per generation after generation 6 (I = 9.9 OR + 148.6 ES, G 6-11, $P < 0.005$). Responses for MUM in Line C were 0.18 ± 0.05 pigs per generation before generation 5 ($P < 0.05$) and -0.14 ± 0.05 pigs per generation after generation 5 ($P < 0.05$).

Pigs Per Litter

Estimated genetic and phenotypic trends for number of fully form pigs, pigs born alive, stillborn pigs and mummified pigs per litter in L2, L4, L5 and L45 are

given in Figures 17.1-17.8. The large genetic and phenotypic correlations between FF and BA (Table 19.1) explain why FF and BA have similar genetic and phenotypic trends. Direct and indirect selection on BA increased FF and BA. However, selection for OR and ES in L2 genetically improved FF linearly but quadratic genetic responses occurred for BA (G 0-11, $P < 0.01$). Selection for OR and ES in L2 genetically increased SB linearly but quadratic genetic responses occurred for MUM (G 0-11, $P < 0.01$). Selection on for OR resulted in dams with a uterus that cannot nurture as many fetuses as the number of ova shed. Thus, uterine capacity was limiting number of live pigs at birth and causing more SB and MUM pigs, consistent with the model of OR and uterine capacity described by Bennett and Leymaster (1990).

Index weight on ES during selection for OR and ES in G 6-11 was about twice that of the weight during G 0-5, whereas of the weight on OR was similar in both periods. The net effect was that correlated response for MUM increased in the first period and decreased in the second period. Similarly, BA increased faster for L5 than L4 because prior selection increased OR in L2 without a concomitant increase in ES. Therefore, two-stage selection for OR and LS in L4 was unbalanced selection, placing too much emphasis on OR and too little on LS, a measure of uterine capacity in high ovulating females. However, in L5, which began from with a lower OR than L4, Two-stage selection appeared to be more balanced, placing approximately optimum selection pressure on both OR and uterine capacity, resulting in rapid increase in both BA and Ff pigs per litter. Selection for BA, WT, BF and LMA, correlated genetic

responses for BA in L2 and L45 were similar to correlated genetic responses for FF; correlated genetic responses for MUM was slightly increased in L45 but was near zero in L2; correlated genetic responses for SB were slightly decreased in L2 and L45.

Age of Puberty

Estimated genetic and phenotypic trends for age of puberty by line are given in Figures 18 and 19, respectively. Genetic and phenotypic responses for AP in L2, L4 and L5 decreased as number of pigs born alive increased ($P < 0.01$). Correlated genetic and phenotypic responses for AP in L4 and L5 were decreased faster than that in L2. L4 and L5 had similar correlated genetic and phenotypic responses for AP.

Litter Birth Weight, Litter Weaning Wright and Pigs Weaned

Estimated genetic trends for litter birth weight by line are given in Figure 20. Selection for OR and ES in L2 slightly increased LBW ($P < 0.1$). Two-stage selection for OR and LS in L4 and L5 (G 8-16, $P < 0.01$) increased LBW more rapidly than direct selection for FF in L2 (G 12-14, $P < 0.05$). When selected for BA and BW, correlated selections for LBW responses in L5 were larger than that in L2 and L4 (L5 > L4 > L2). When selected for BA, WT, BF and LMA, correlated responses in L2 and L45 were similar ($P < 0.01$).

Estimated phenotypic trends for litter birth weight by line are given in Figure

21. When selection for OR and ES in L2, LBW decreased ($P < 0.05$). When the selection objective in L2 changed from OR and ES to FF (G 12-14), to BA and BW (G 15-19) and to BA, WT, BF and LMA (G 20-28), the phenotypic mean each generation for G 12-28 was larger than that for selection on OR and ES (G 0-11). When selected for BA, WT, BF and LMA, correlated responses in LBW in L2 increased ($P < 0.05$).

The large genetic correlations between FF and LBW (Table 19.1) explain why FF and LBW have similar genetic and phenotypic trends. Phenotypic responses in FF in L2 increased linearly but responses in LBW were linear for G 0-11 and quadratic for G 12-27.

Estimated genetic trends for litter weaning weight by line are given in Figure 22. Negative, linear genetic responses in LWW in L2 occurred before Generation 22, but increased after Generation 22. When dams were measured at 12 d, the genetic response for LWW in L4 decreased (G 12-21, $P < 0.05$). When dams were measured at 18 d, the genetic response for LWW in L2 and L45 increased (G 22-27, $P < 0.05$).

Estimated phenotypic trends for litter weaning weight by line are given in Figure 23. The phenotypic mean for LWW was affected by different weaning age measured. A t-test did not provide evidence that LWW was changed when pigs had similar weaning age, except when measured at 28 d in L2 ($P < 0.01$). The phenotypic response for LWW in L2 decreased 0.875 ± 0.196 kg/litter per generation

(G 0-11, P $<$ 0.01).

Estimated genetic trends for number of pigs weaned by line are given in Figure 24. The genetic trend for NW was similar to the genetic trend for LWW in L2, L4 and L45. When LWW of dams were measured at similar age, the genetic trends for NW in all lines were similar, and the genetic responses for NW were small in all lines.

Estimated phenotypic trends for number of pigs weaned by line are given in Figure 25. There is no evidence that NW, after adjustment to a standard number nursed and a standard weaning age, is affected by any set of selection traits. The phenotypic response for NW in L5 increased 0.221 ± 0.086 pigs/litter per generation (G 12-21, P $<$ 0.05). The phenotypic response for NW in L45 increased 0.385 ± 0.136 pigs/litter per generation (G 22-27, P $<$ 0.1).

Birth Weight and Weaning Weight

Estimated genetic trends and maternal genetic trends for birth weight by line are given in Figures 26 and 27. Estimated direct and maternal genetic trends for birth weight in lines C and 2 and in lines C, 4, 5 and 45 are given in Figures 28.1 and 28.2. Direct genetic response for BW in L2 was slightly decreased at the first 14 generations. When Selection for OR and LS, direct genetic response for BW was slightly increased in L4 but was slightly decreased in L5 (P $<$ 0.01). Selection for BA, WT, BF and LMA slightly increased direct genetic responses for BW in L2 and L45 (P $<$ 0.01). Direct genetic means of BW on each generation in L4, L5 and L45

were larger than that in L2. Direct or indirect selection for BA linearly decreased maternal genetic responses for BW in L2, L5 and L45. Direct and maternal genetic responses for BW under any set of selection traits were less than 0.02 kg per generation in all lines.

Estimated phenotypic trends for birth weight by line are given in Figure 29. Because maternal heritability for BW is about twice greater than direct heritability, phenotypic trends for BW is expected to be more like maternal genetic trends than direct genetic trends. Phenotypic response for BW in L2 decreased for the first 19 generations with a near zero response for G 20-28. Selection for OR and LS (G8-16) and BA and BW (G17-19) decreased BW in L5 faster than that in L4. Phenotypic responses for BW under any set of selection traits were less than 0.03 kg per generation in all lines.

Estimated genetic trends and maternal genetic trends for weaning weight by line are given in Figures 30 and 31. Estimated direct and maternal genetic trends for weaning weight in lines C and 2 and in lines C, 4, 5 and 45 are given in Figures 32.1 and 32.2. Both means of direct and maternal genetic responses in all lines were affected by measured weaning age. Under any set of selection practice, direct and maternal genetic responses for WW were small when pigs had similar weaning age. Direct or maternal genetic responses for WW under any set of selection traits were less than 0.03 kg per generation in all lines.

Estimated phenotypic trends for weaning weight by line are given in Figure 33.

Phenotypic means for WW were similar in all lines when they were measured at similar age, except there was slightly decrease response in L2 for the first 11 generations.

Weight at 180 d of age, Backfat of the 10th rib, Average Backfat and Longissimus Muscle Area

Estimated genetic trends and maternal genetic trends for weight at 180 d of age by line are given in Figures 34 and 35. Estimated direct and maternal genetic trends for weight at 180 d of age in lines C and 2 and in lines C, 4, 5 and 45 are given in Figures 36.1 and 36.2. Index selection for OR and ES (G 0-11) decreased more direct genetic responses for WT than direct selection for FF (G 12-14) in L2. Direct genetic responses for WT in L4 increased faster than that in L5, when lines were selected for OR and LS (G 8-16, L4 > L5). Selection for BA and BW in L2 result in direct genetic response for WT of 0.54 ± 0.10 kg per generation (G15-19, $P < 0.01$). Selection for BA and BW in L4 and L5 increased WT (G 17-19, $P < 0.1$). Moderate and positive genetic correlations of WT with BW ($r_a = 0.27$) and low and positive genetic correlations of WT with BA ($r_a = 0.08$) may explain why WT was increased when L2, L4 and L5 were selected for BA and BW. Selection for BA, WT, BF and LMA increased WT 1.81 ± 0.24 kg/generation in L2 and 1.55 ± 0.18 kg/generation in L45 ($P < 0.01$). High and positive genetic correlations of WT with LMA ($r_a = 0.53$), low and positive genetic correlations of WT with BA ($r_a = 0.08$), moderate direct

heritability for WT (h_a^2 = 0.36) and low maternal heritability for WT (h_m^2 = 0.05) may explain why WT had great increases when L2 was selected for BA, WT, BF and LMA. Maternal genetic responses for WT increased in L2 for G 0-11 ($P < 0.01$) and G 15-19 ($P < 0.05$), in L4 for G8-16 ($P < 0.05$) and in L45 for G20-28 ($P < 0.01$). Changes of maternal genetic responses for WT under any set of selection traits were less than 0.2 kg per generation in all lines.

Estimated phenotypic trends for weight at 180 d of age by line are given in Figure 37. Selection for OR and ES in L2 increased phenotypic responses for WT of 0.38 ± 0.19 kg/generation (G 0-11, $P < 0.1$). Selection for BA, WT, BF and LMA in L2 increased phenotypic responses for WT of 1.28 ± 0.64 kg/generation (G 20-28, $P < 0.1$) but selection for OR and LS in L5 decreased phenotypic responses for WT of 1.02 ± 0.40 kg/generation (G 8-16, $P < 0.05$).

Estimated genetic trends for backfat depth of the 10th rib with a covariate of age and of final weight at 180 d of age by line are given in Figures 38 and 39. Estimated phenotypic trends for backfat depth of the 10th rib at 180 d of age by line are given in Figure 40. Selection for BA, WT, BF and LMA in L2 and L45 resulted in similar genetic response for BF in model with a covariate of age and model with a covariate of final weight. There is no evidence that genetic response for BF decrease in L2 ($P < 0.1$). Selection for BA, WT, BF and LMA in L45 decreased genetic responses for BF in model with a covariate of age ($P < 0.01$) and model with a covariate of final weight ($P < 0.01$). There is no evidence that phenotypic response

for BF decrease in L2 and L45 ($P < 0.1$).

Estimated genetic trends for average backfat depth with a covariates of age and of final weight at 180 d of age by line are given in Figures 41 and 42. Estimated phenotypic trends for average backfat depth at 180 d of age by line are given in Figure 43. Selection for BA, WT, BF and LMA in L2, L4 and L5 resulted in similar genetic response for ABF in model with a covariate of age and model with a covariate of final weight. Selection for OR and LS slightly increased genetic responses for ABF in L4 ($P < 0.01$) and L5 ($P < 0.01$). Selection for OR and LS increased phenotypic responses for ABF 0.090 ± 0.022 cm/generation in L4 ($P < 0.01$) and 0.089 ± 0.013 cm/generation in L5 ($P < 0.01$).

Estimated genetic trends for longissimus muscle area with a covariate of age, of final weight and of final weight and random maternal genetic effects at 180 d of age by line are given in Figures 44, 45 and 46. Estimated direct and maternal genetic trends for longissimus muscle area with a covariate of final weight and random maternal genetic effects at 180 d of age by line are given in Figure 47. Estimated phenotypic trends for longissimus muscle area at 180 d of age by line are given in Figure 48. Selection for BA, WT, BF and LMA increased direct genetic responses for LMA in L2 ($P < 0.01$) and L5 ($P < 0.01$) in three set of models, but slightly decreased maternal genetic responses for LMA in L2 ($P < 0.01$) and L45 ($P < 0.05$) in model with a covariate of final weight and maternal genetic effects. However, selection for BA, WT, BF and LMA decreased phenotypic responses for LMA 0.695 ±

0.437 cm/generation in L2 ($P < 0.05$) and decreased LMA 0.969 ± 0.295 cm/generation in L45 ($P < 0.05$).

Difference in Genetic and Phenotypic Mean Between Selection and Control Lines

Coefficients (b) and SE for regression of difference in mean direct and maternal breeding values on generation between selection and control line by trait are given in Tables 25.1 and 25.2. Coefficients (b) and SE for regression of difference in phenotypic mean on generation between selection and control line by trait are given in Tables 26.1 and 26.2. Regression of difference in direct breeding values on generation between all selection lines and control line were significant for most traits ($P < 0.1$). Although regression of difference in direct breeding values on generation between L2 and LC was not significant for WT during G 0-28, regression of differences was significantly decreased WT 0.35 ± 0.04 kg/generation during G 0-14 and significantly increased WT 0.93 ± 0.14 kg/generation during G 15-27. Regression of difference in maternal breeding values on generation between all selection lines and control line were significant for BW in L2 and L4, WW (G 0-28) in L4 and L45, WW at 28 d in L2, WW at 12 d in L4 and L5, WW at 18 d in L2 and L45 and WT in L2 ($P < 0.1$). Regression of difference in phenotypic mean on generation between selection lines and LC was significant for most reproduction traits ($P < 0.1$).

Investigate A Plateau in Responses for Number of Pigs Born Alive Per Litter

Significant linear and quadratic regression coefficients for cumulative selection differential on generation, for mean EBVs on generation, and estimates of genetic variance for number of pigs born alive by selection lines and traits are given in Table 27. Both selection lines 2 and 45 still exhibit genetic variances of BA during G 20-28. During G 20-28, the linear regression coefficient for CSD was significant for BA in L2 and L45 but the quadratic regression coefficient for CSD was not significant for BA in L2 and L45 ($P < 0.01$). During G 20-28, a linear effect of mean EBVs was significant for BA in L2 and L45, but a quadratic effect of mean EBVs was not significant for BA in L2 and L45 ($P < 0.01$). Thus, after 28 generations of main selection for BA, a plateau has not been reached in L2 and L45.

Chapter 5

Discussion

Inbreeding effects were significant but were not included in the analyses, because inbreeding effects were not considered when selections were practiced. Maternal genetic effects for BW, WW and WT have been tested and considered in the analyses. Previous analyses for part of this population have showed that litter effects (Johnson *et al.*, 1999; Ruiz-Flores and Johnson, 2001; Petry and Johnson, 2004; Hsu. et al., 2010) and pen-mates effects (Hsu. et al., 2010) should be included in the models. Those results are in agreement with Rosendo *et al.* (2007c) for maternal effects, with Noguera *et al.* (2002), Mesa *et al.* (2005) and Rosendo *et al.* (2007a, 2007b and 2007c) for litter effects and with Cassady and Van Vleck (2004), Arango *et al.* (2005b), Bergsma *et al.* (2008) and Chen *et al.* (2008).

Direct heritability for BA is similar to Rosendo *et al.* (2007b) and a little greater than Holl and Robison (2003), Holm *et al.* (2004) and Arango *et al.* (2005a). Direct heritability for FF is similar to Mesa *et al.* (2005). Direct heritability for OR is similar to Blasco et al. (1998), Blasco *et al.* (2005) and Rosendo *et al.* (2004a) on the left, right and both ovaries at puberty, but is smaller than estimates of realized heritability of Zimmerman and Cunningham (1975) and Cunningham *et al.* (1979), but is a little greater than Neal *et al.* (1989). Direct heritability for ES is similar to Neal *et al.* (1989). Low direct heritability for SV is similar to Neal *et al.* (1989), Holm *et al.* (2004), Blasco et al. (1998), Blasco *et al.* (2005), Rosendo *et al.* (2007c). Young

et al. (1978) found much greater direct heritability for OR, BA and FF than this study. High direct heritability for AP is greater than Holm *et al.* (2004), Rosendo *et al.* (2007b). Low direct heritability for BW is similar to estimates of Fredeen and Mikami (1986c), Chen *et al.* (2003), Mesa *et al.* (2005) and Rosendo *et al.* (2007c). Low direct heritability for WW is similar to estimates of Fredeen and Mikami (1986c), Chen *et al.* (2003) and Rosendo *et al.* (2007c). Moderate direct heritability for BF is similar to estimates of Chen *et al.* (2003) and Arango *et al.* (2005a), but greater than estimate of Cleveland *et al.* (1988) and Rosendo *et al.* (2007c), and smaller than estimates of Holm *et al.* (2004). Moderate direct heritability for LMA is similar to estimates of Chen *et al.* (2003) and Holm *et al.* (2004), but smaller than estimate of Cleveland *et al.* (1988).

The genetic and phenotypic correlations of OR, ES and SV at 30 d of gestation with BW, WW, LWW and WT in Young *et al.* (1977) are very different from estimates of OR, ES and SV at 50 d of gestation in this study. Some genes affect OR, ES and SV in the breeds of Young *et al.* (1977) may have larger effects on above growth traits (BW, WW, LWW and WT) than those genes in the breeds of this experiment.

Selection for ovulation rate caused a decrease in embryo survival and fetus survival, which is in agreement with Cunningham et al. (1979), Johnson et al. (1999), Ruiz-Flores and Johnson (2001) Petry and Johnson (2004) and the models of Bennet and Leymaster (1989). However, the negative estimate of genetic correlation between OR and SV is greater than all estimates of Rosendo *et al.* (2007a). Moderate to high

positive genetic and phenotypic correlations of OR with SV in Blasco *et al.* (2005) for rabbit have opposite estimates to this study. The limit of uterine capacity maybe was not reached in the experiment of Blasco *et al.* (2005). Uterine overcrowding from high OR may be a reason to cause high negative correlation between OR and SV. Estimates of genetic correlations of OR with FF are small and positive and similar to the estimates of Cunningham *et al.* (1979) and Rosendo *et al.* (2007a). Estimate of genetic correlation between OR and BA is small and negative, but the estimate of Rosendo *et al.* (2007b) is moderate and positive, but the estimate of Cunningham *et al.* (1979) is small and positive. Again, this may be because of different relationships of OR and uterine capacity in the studies. When OR exceeds uterine capacity, then negative correlations are expected. However, if OR is less than uterine capacity, then positive associations between the traits is expected (Bennet and Leymaster, 1989).

Cunningham *et al.* (1979) obtained genetic correlations of OR with NW and LBW and LWW which are opposite to the estimates of this study. Rosendo *et al.* (2007b) obtained very high genetic and phenotypic correlations between BA and NW which are very different from estimates of this study. This result can be expected because this study has small negative relationship between OR and BA, but estimate of Cunningham *et al.* (1979) and Rosendo *et al.* (2007b) are positive. Again, these relatiohsips are dependent on the balance between OR and uterine capacity, which determine litter size at birth, in the populations studied.

The estimate of genetic correlation of SV with FF is small and positive

whereas the estimate of Rosendo *et al.* (2007a) is high and positive. Estimate of genetic correlation between SV and BA is moderate and the estimate of Rosendo *et al.* (2007a) is high.

Estimates of genetic and phenotypic correlations of BA with FF are similar to the estimate of Young *et al.* (1978). Estimates of genetic and phenotypic correlations of BA and LBW are similar to the estimates of Young *et al.* (1978) and Rosendo *et al.* (2007b).

Almost independent genetic correlation between OR and BW is different from moderately negative correlation obtained by Rosendo *et al.* (2007b). Moderately negative genetic correlation between SV and BW is similar to estimate of Rosendo *et al.* (2007b). Almost independent genetic correlation between FF and BW is different from moderately negative correlation obtained by Mesa *et al.* (2005). Almost independent genetic correlation between BA and BW is different from moderately negative correlation obtained by Rosendo *et al.* (2007b). The results indicate that genes affected BW in this study have very small effects on above reproductive traits.

Direct-maternal genetic correlations for BW and WW are all negative (-0.21 ~ -0.68) in Rosendo *et al*. (2007c) but direct-maternal genetic correlations of this study is 0.13 for BW and are -0.06, 0.00 and 0.98 for WW at 28d, at 12 d and at 18d.

Reproductive traits have small effects on growth and carcass traits which are also reported by Young *et al.*, (1977), Young *et al.*, (1978), Fredeen and Mikami (1986b), Cleveland. (1988), Estany et al. (2002), Noguera *et al.* (2002), Chen *et al.*

(2003), Holl and Robison (2003), Holm *et al.* (2004), Petry *et al.* (2004), Arango *et al.* (2005a) and Rosendo *et al.* (2007c). This indicates that selection for reproduction, growth and carcass traits would not expected to have large effects on reproductive traits with growth and carcass traits.

The results of this study showed that direct and indirect selection on components of litter size can improve litter size, and the results are in agreement with Johnson et al. (1984), Neal et al. (1989), Bennett and Leymaster (1989; 1990a; 1990b), Johnson et al. (1999), Ruiz-Flores and Johnson (2001), Rosendo et al. (2007a). Genetic responses for age of puberty were decreased by index selection on ovulation rate and embryo survived or two stages selection for ovulation rate and litter size (Ruiz-Flores and Johnson, 2001). Genetic responses for number of pigs born alive ($P < 0.05$), number of fully formed pigs ($P < 0.05$) and litter birth weight ($P < 0.1$) were increased over 28 generations selections (selection line – control line). Genetic responses for weaning weight did not have many changes over 28 generations selections (selection line – control line, $P < 0.05$).

Number of fully formed pigs can be improved by index selection on ovulation rate and embryo survived, but number of stillborn pigs will also increase, which agrees with Bennett and Leymaster (1990b). Number of pigs born alive can be improved by index selection on ovulation rate and embryo survived, which is in agreement with Bennett and Leymaster (1990b), but the limit of uterine capacity will stop increasing of number of pigs born alive (Bennett and Leymaster, 1990a; Blasco

et al., 2005; Santacreu et al., 2005). Much higher economic values on embryo survived than ovulation rate may decrease number of mummified pigs, when index selection for ovulation rate and embryo survived (Johnson et al., 1999). Index selection for ovulation rate and embryo survival increased direct genetic responses for ovulation rate, embryo survival, number of pigs born alive, number of fully formed pigs, number of mummified pigs, number of stillborn pigs, litter birth weight ($P < 0.1$), and slightly decreased genetic responses for embryo survival rate, age of puberty, litter weaning weight, number of pigs weaned, individual birth weight, final weight at 180 d of age and average backfat ($P < 0.1$), and slightly decreased maternal genetic responses for individual birth weight, individual weaning weight and final weight at 180 d of age ($P < 0.05$).

Although several authors reported that direct selection for increased litter size have not significant or small responses (Ollivier, 1982; Haley et al., 1988; Bolet et al., 1989, Pérea-Enciso and Bidanel, 1997, Estany et al., 2002; Holl and Robison, 2003) in swine and in mice (Bakker et al., 1878). Selection for ovulation rate and embryo survived, direct selection for number of fully formed pigs or two stages selection for ovulation rate and litter size can improve litter size, which is in agreement with (Lamberson et al., 1991; Johnson et al., 1999). Selection on number of fully formed pigs or index selection on ovulation rate and litter size after reaching the limit of uterine capacity can continue to improve number of pigs born alive. Genetic response for number of pigs born alive is less after selection for ovulation rate and embryos

survived than after random selection. Two stages selection for ovulation rate and litter size increased direct genetic responses for number of pigs born alive, number of fully formed pigs, number of stillborn pigs, litter birth weight, weight at 180 d of age and average backfat at 180 d of age, but decreased direct genetic responses for age of puberty ($P < 0.1$). Direct selection on number of litter size is efficiency which also agrees with Sorensen et al. (2000), Noguera et al. (2002) and Tribout et al. (2003). Direct selection for fully formed pigs increased direct genetic responses for number of pigs born alive, number of fully formed pigs, litter birth weight, but decreased direct genetic responses for number of mummified pigs, litter weaning weight and weight at 180 d of age ($P < 0.1$).

Kerr and Cameron (1995), Arango et al. (2005a), Canario et al., (2006) and Rosendo et al. (2007b) reported that selection for litter size would be expected to decrease piglet birth weight and decrease piglet survival. Their reports agree with slightly decreasing birth weight at first 14 generation in L2 and at first 16 generations in L5. After selection strategy was changed to select for number of pigs born alive and birth weight, however, number of pigs born alive was improved and birth weight was slightly increased. Selection for number of pigs born alive and birth weight in L2 also increased direct genetic responses for number of fully formed pigs, litter birth weight and final weight at 180 d of age, and slightly decreased direct genetic response for number of mummified pigs and individual weaning weight ($P < 0.1$); in L4 slightly increased direct genetic responses for litter weaning weight, individual birth weight

and final weight at 180 d of age, and slightly decreased direct genetic responses for number of stillborn pigs ($P < 0.1$); in L5 also increased direct genetic responses for number of pigs born alive, number of fully formed pigs, litter birth weight and final weight at 180 d of age ($P < 0.1$).

Chen et al. (2003), Holm *et al.* (2004) and Arango et al. (2005a) concluded that long-term selection for productive traits may result in significant effects on reproductive traits. Estany et al. (2002) concluded that long-term selection for litter size may result in significant effects on lean growth. However, the result of selected 28 generations for number of pigs born alive, and selected for number of pigs born alive, final weight at 180 d of age, backfat of the 10^{th} rib and longissimus muscle area at the last eight generation still showed favorable genetic responses for those traits. Number of pigs born alive did not have large effects on final weight at 180 d of age, backfat of the 10^{th} rib and longissimus muscle area at the last eight generations. Genes affected number of pigs born alive in this population may not have many genes affected growth traits. Selection on pigs born alive, final weight at 180 d of age, backfat and longissimus muscle area increased final weight after final weight had decreased because of litter size selection. Selection on number of pigs born alive, final weight at 180 d of age, backfat of the 10^{th} rib at 180 d of age and longissimus muscle area at 180 d of age increased direct genetic responses for number of pigs born alive, number of fully formed pigs, litter birth weight, individual birth weight, final weight at 180 d of age, longissimus muscle area at 180 d of age, and increased maternal

genetic responses for individual weaning weight, but decreased maternal genetic responses for longissimus muscle area in L2 and L45 ($P < 0.05$); In L45, direct genetic responses for number of mummified pigs, litter weaning weight, number of pigs weaned and individual weaning weight and maternal genetic responses for final weight at 180 d of age were also increased, and direct genetic responses for backfat of the 10^{th} rib was decreased ($P < 0.01$).

The trends of cumulative selection differentials for ovulation rate, embryo survival, number of pigs born alive, number of fully formed pigs, birth weight, final weight and longissimus muscle area at 180 d of age were linear or quadratic increases and for bachfat of the 10^{th} rib at 180 d of age was linear decreases in all selection line. The trends of cumulative selection differentials for those traits are similar to genetic trends, except for birth weight and bachfat of the 10^{th} rib. Response for bachfat of the 10^{th} rib was consistent with L45 but less selection applied to bachfat of the 10^{th} rib in L2. Selection applied to birth weight was less, because selection differential in some generation was negative.

At the last eight generations, the linear effects of cumulative selection differentials and mean EBVs were significant for number of pigs born alive in L2 and L45, and the quadratic effects of cumulative selection differentials and mean EBVs were not significant for number of pigs born alive in L2 and L5 ($P < 0.01$). The selection lines still have genetic variances remaining in number of pigs born alive. After 28 generations of selection, a plateau in response for number of pigs born alive

has not been reached in this experiment.

Greater and longer-term response from epistatic gene action (Jannink, 2003) may explain why the results still show increasing genetic and phenotypic trends in number of pigs born alive over direct and indirect selections of 28 generations (years). Changed selection strategies could bring increases. However, the epistatic gene actions could also bring some or more changes to additive genetic variances and selection responses. Although it is complicated to estimate epistatic variance, estimate of epistatic variance is also helpful to get more accurate selection responses, especially for polygenic traits or special mating strategy. Marker assisted selection have been applied into traditional index selection in swine. If makers related to epistatic effects can be detected and developed, the genetic selection is be expected to improve responses. Selection on pigs born alive, final weight, backfat and longissimus muscle area with appropriate economic values and appropriate diet in different growth periods is be expected to increase number of pigs born alive, growth rate, lean and decrease backfat in future generations.

Table 1. **Number of observations (n), unadjusted means, standard deviations (SD), and ranges for traits**

Trait[a]	n	Mean	SD	Minimum	Maximum
BA, pig	5403	9.89	3.27	0	22
OR, ova	3298	16.35	5.00	4	79
ES, embryo	1883	11.93	3.05	1	22
SV, %	1883	0.73	0.19	0.02	2.75
AP, day	4842	179.07	26.68	123	304
FF, pig	5403	11.12	3.66	0	23
MUM, pig	5403	0.45	1.00	0	13
SB, pig	5403	1.23	1.94	0	19
LBW, kg	5397	12.51	3.66	0.60	27.16
LWW, kg	5131	36.53	15.80	1.72	138.20
LWW (28d), kg	1594	53.47	13.24	4.40	138.20
LWW (12d), kg	2661	26.67	8.13	1.72	65.91
LWW (18d), kg	876	35.65	11.16	2.35	79.53
NW, pig	5272	8.43	2.53	0	22
NW (28d), pig	1627	8.40	2.24	0	22
NW (12d), pig	2753	8.50	2.69	0	21
NW (18d), pig	892	8.31	2.51	0	19
BW, kg	54174	1.13	0.28	0.15	2.40
WW, kg	43077	4.29	1.79	0.22	15.90
WW (28d), kg	14532	6.24	1.34	1.18	15.90
WW (12d), kg	21169	2.98	0.72	0.26	5.85
WW (18d), kg	7376	4.21	1.08	0.22	11.42
WT, kg	13714	91.70	12.62	30.40	138.50
BF, cm	5796	2.12	0.50	0.80	4.57
ABF, cm	7683	2.11	0.47	0.80	4.32
LMA, cm^2	5797	29.42	4.85	9.05	52.49

[a] Trait: BA = number of pigs born alive; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; FF = number of fully formed pigs; MUM = number of mummified pigs; SB = number of stillborn pigs; LBW = litter birth weight; LWW = litter weaning weight for generations 0-27; ; LWW(28d), LWW(12d) or LWW(18d) = litter weaning weight at 28 d for generations 0-11, at 12 d for generations 12-21 or at 18 d for generations 22-27; NW(28d), NW(12d) or NW(18d) = number of pigs weaned at 28 d for generations 0-11, at 12 d for generations 12-21 or at 18 d for generations 22-27; BW = birth weight; WW(28d), WW(12d) or WW(18d) = weaning weight at 28 d for generations 0-12, at 12 d for generations 13-22 or at 18 d for generations 23-28; WT = final weight at 180 d of age ; BF = backfat depth of the 10^{th} rib at age of final weight included a fixed covariate of age or a fixed covariate of final weight; ABF = average backfat depth at age of final weight included a fixed covariate of age or a fixed covariate of final weight; LMA = longissimus muscle area at age of final weight included a fixed covariate of age, a fixed covariate of final weight or a fixed covariate of final weight and a random maternal genetic effect.

Table 2. **Unadjusted means, standard deviations (SD) and ranges for traits with the covariates of age (day), number of pigs nursed (pig) or final weight (kg)**

Trait[a]	Mean	SD	Minimum	Maximum
		Age		
LWW, kg	17.47	7.01	6	38
LWW (28d), kg	27.13	2.26	19	38
LWW (12d), kg	11.76	1.34	6	16
LWW (18d), kg	17.26	2.04	12	31
NW, pig	17.45	7.00	6	38
NW (28d), pig	27.15	2.24	19	38
NW (12d), pig	11.77	1.32	6	18
NW (18d), pig	17.27	2.03	12	31
WW, kg	17.98	7.14	5	43
WW (28d), kg	27.26	2.27	18	43
WW (12d), kg	11.85	1.35	5	16
WW (18d), kg	17.30	2.03	12	31
WT, kg	178.69	10.94	140	261
BF, cm	180.55	10.03	146	227
ABF, cm	177.21	11.07	140	229
LMA, cm^2	180.55	10.02	146	227
		Number of Pigs Nursed		
LWW, kg	10.23	2.43	1	25
LWW (28d), kg	9.69	2.01	1	23
LWW (12d), kg	10.44	2.50	1	25
LWW (18d), kg	10.59	2.70	1	23
NW, kg	10.06	2.66	1	25
NW (28d), kg	9.54	2.26	1	23
NW (12d), kg	10.24	2.75	1	25
NW (18d), kg	10.45	2.88	1	23
		Final Weight		
BF, cm	94.53	12.76	40.4	138.5
ABF, cm	89.71	11.83	31.6	129.5
LMA, cm^2	94.53	12.76	40.4	138.5

[a] Traits: LWW, LWW(28d), LWW(12d) or LWW(18d) = litter weaning weight for G 0-27, at 28 d for G 0-11, at 12 d for G 12-21 or at 18 d for G 22-27; NW, NW(28d), NW(12d) or NW(18d) = number of weaning pigs for G 0-27, at 28 d for G 0-11, at 12 d for G 12-21 or at 18 d for G 22-27; WW, WW(28d), WW(12d) or WW(18d) = weaning weight for G 0-28, at 28 d for G 0-12, at 12 d for G 13-22 or at 18 d for G 23-28; WT = final weight at 180 d; BF = backfat depth of the 10^{th} rib at age of WT included a covariate of age or a covariate of WT; ABF = average backfat depth at age of WT included a covariate of age or a covariate of WT; LMA = longissimus muscle area at age of WT included a covariate of age, a covariate of WT or a covariate of WT and a random maternal genetic effect.

Table 3. **Number of levels for fixed effects and uncorrelated random effects for each trait[a]**

	Fixed Effects[b]					Random Effects[c]	
Traits[d]	**ctg**	**sex**	**age**	**nns**	**wt**	**lit**	**pen**
BA	48	~	~	~	~	3102	~
OR	18	~	~	~	~	1144	~
ES	11	~	~	~	~	702	~
SV	11	~	~	~	~	702	~
AP	24	~	~	~	~	1796	~
FF	48	~	~	~	~	3102	~
MUM	48	~	~	~	~	3102	~
SB	48	~	~	~	~	3102	~
LBW	48	~	~	~	~	3101	~
LWW (28d)	17	~	Cov (Q)	Cov (Q)	~	992	~
LWW (12d)	20	~	Cov (Q)	Cov (Q)	~	1489	~
LWW (18d)	11	~	Cov (Q)	Cov (Q)	~	532	~
NW (28d)	17	~	Cov (Q)	Cov (Q)	~	1003	~
NW (12d)	20	~	Cov (Q)	Cov (Q)	~	1513	~
NW (18d)	11	~	Cov (Q)	Cov (Q)	~	539	~
BW	50	2	~	~	~	5225	~
WW (28d)	19	2	Cov (Q)	~	~	1717	~
WW (12d)	20	2	Cov (Q)	~	~	2541	~
WW (18d)	11	2	Cov (Q)	~	~	905	~
WT	49	2	Cov (L)	~	~	3857	111
BF(age)	20	2	Cov (L)	~	~	1520	103
ABF(age)	29	2	Cov (L)	~	~	2323	41
LMA(age)	20	2	Cov (L)	~	~	1520	103
BF(WT)	20	2	~	~	Cov (L)	1520	103
ABF(WT)	29	2	~	~	Cov (L)	2323	41
LMA(WT)	20	2	~	~	Cov (L)	1520	103
LMA(WT&M)	20	2	~	~	Cov (L)	1520	103

[a] " ~ " indicates not included; " Cov (L) and/or Cov (Q)" indicates linear and/or quadratic regression on a covariate; [b] Fixed effects: ctg = contemporary group; sex = gender; age, nns or wt = covariate for age, number of pigs nursed or final weight. [c] Uncorrelated random effects: lit or pen = litter or pen-mate effects. [d] Traits: BA, FF, MUM or SB = number of pigs born alive, fully formed, mummified or stillborn pigs; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; LBW = litter birth weight; LWW(28d), LWW(12d) or LWW(18d) = litter weaning weight at 28, 12 or 18 d; NW(28d), NW(12d) or NW(18d) = number of pigs weaned at 28, 12 or 18 d; BW = birth weight; WW(28d), WW(12d) or WW(18d) = weaning weight at 28, 12 or 18 d; WT = final weight at 180 d; BF(age) or BF(WT) = backfat of the 10^{th} rib with a covariate of age or of WT; ABF(age) or ABF(WT) = average backfat with a covariate of age or WT; LMA(age), LMA(WT) or LMA(WT&M) = longissimus muscle area with a covariate of age, WT or WT and a random maternal genetic effect.

Table 4. **Number of sires with litter records by line for each generation**

Generations	Lines[a]							
	L1	**L2**	**L4**	**L5**	**L6**	**L45**	**L16**	**L61**
-1	19		~	~	~	~	~	~
0	15	15	~	~	~	~	~	~
1	14	20	~	~	~	~	~	~
2	15	18	~	~	~	~	~	~
3	15	18	~	~	~	~	~	~
4	15	19	~	~	~	~	~	~
5	15	19	~	~	~	~	~	~
6	15	18	~	~	~	~	~	~
7	15	19	~	~	~	~	~	~
8	15	18	~	~	~	~	~	~
9	15	21	~	~	~	~	~	~
10	15	17	14	15	15	~	~	~
11	15	20	15	15	14	~	~	~
12	16	15	16	15	13	~	~	~
13	16	14	14	16	15	~	~	~
14	16	15	15	14	14	~	~	~
15	14	18	14	15	15	~	~	~
16	15	18	15	15	15	~	~	~
17	15	14	15	14	15	~	~	~
18	15	16	16	15	15	~	~	~
19	15	15	14	16	15	~	~	~
20	15	16	19	15	18	~	~	~
21	16	15	~	~	14	18	~	~
22	18	30	~	~	~	15	14	~
23	~	29	~	~	~	16	13	15
24	~	29	~	~	~	14	14	14
25	~	15	~	~	~	16	14	15
26	~	15	~	~	~	16	14	15
27	~	15	~	~	~	15	12	14
28	~	14	~	~	~	~	14	~

[a] Lines:

L1, L6, L16 and L61 = control lines; L2, L4, L5 and L45 = selection lines.

Table 5. **Number of dams with litter records by lines in each generation**

Generations	Lines[a]							
	L1	**L2**	**L4**	**L5**	**L6**	**L45**	**L16**	**L61**
-1	45		~	~	~	~	~	~
0	82	42	~	~	~	~	~	~
1	41	43	~	~	~	~	~	~
2	40	43	~	~	~	~	~	~
3	42	44	~	~	~	~	~	~
4	42	44	~	~	~	~	~	~
5	43	44	~	~	~	~	~	~
6	43	48	~	~	~	~	~	~
7	44	44	~	~	~	~	~	~
8	41	45	~	~	~	~	~	~
9	42	51	~	~	~	~	~	~
10	36	47	44	38	41	~	~	~
11	39	53	52	54	38	~	~	~
12	47	60	44	45	36	~	~	~
13	41	47	43	42	45	~	~	~
14	47	79	41	43	39	~	~	~
15	43	97	48	44	35	~	~	~
16	47	86	43	45	37	~	~	~
17	81	93	42	42	35	~	~	~
18	74	63	41	49	45	~	~	~
19	60	60	46	47	40	~	~	~
20	58	54	37	46	40	~	~	~
21	86	82	~	~	46	88	~	~
22	34	81	~	~	45	52	43	~
23	~	75	~	~	~	45	39	43
24	~	64	~	~	~	34	35	37
25	~	37	~	~	~	38	32	37
26	~	40	~	~	~	37	44	37
27	~	32	~	~	~	35	41	43
28	~	41	~	~	~	~	44	~

[a] Lines:

L1, L6, L16 and L61 = control lines; L2, L4, L5 and L45 = selection lines.

Table 6. **Means, standard deviations (SD) and ranges for inbreeding coefficients by line and the average inbreeding coefficients by line for each generation**

Generations	Lines[a]							
	L1	**L2**	**L4**	**L5**	**L6**	**L45**	**L16**	**L61**
-1	0	0	~	~	~	~	~	~
0	0	0.003	~	~	~	~	~	~
1	0.003	0.017	~	~	~	~	~	~
2	0.015	0.020	~	~	~	~	~	~
3	0.022	0.037	~	~	~	~	~	~
4	0.034	0.057	~	~	~	~	~	~
5	0.034	0.067	~	~	~	~	~	~
6	0.038	0.063	~	~	~	~	~	~
7	0.054	0.081	~	~	~	~	~	~
8	0.060	0.093	~	~	~	~	~	~
9	0.066	0.105	~	~	~	~	~	~
10	0.081	0.113	0.105	0.084	0.084	~	~	~
11	0.079	0.120	0.117	0.080	0.091	~	~	~
12	0.083	0.135	0.135	0.097	0.104	~	~	~
13	0.096	0.144	0.142	0.110	0.105	~	~	~
14	0.098	0.152	0.150	0.123	0.118	~	~	~
15	0.102	0.165	0.166	0.136	0.120	~	~	~
16	0.111	0.182	0.169	0.141	0.131	~	~	~
17	0.119	0.192	0.194	0.142	0.138	~	~	~
18	0.124	0.196	0.207	0.150	0.145	~	~	~
19	0.135	0.201	0.214	0.159	0.152	~	~	~
20	0.141	0.212	0.229	0.164	0.156	~	~	~
21	0.146	0.224	~	~	0.167	0.037	~	~
22	0.154	0.173	~	~	0.172	0.129	0.098	~
23	0.165	0.211	~	~	~	0.136	0.132	0.097
24	0.166	0.224	~	~	~	0.142	0.140	0.136
25	~	0.227	~	~	~	0.164	0.142	0.153
26	~	0.183	~	~	~	0.173	0.156	0.148
27	~	0.200	~	~	~	0.201	0.167	0.153
27	~	0.226	~	~	~	0.205	0.171	0.164
28	~	0.237	~	~	~	~	0.179	~
Mean	0.085	0.137	0.166	0.126	0.129	0.148	0.148	0.142
SD	0.054	0.070	0.046	0.040	0.033	0.059	0.030	0.028
Minimum	0	0	0	0	0.001	0	0.001	0.001
Maximum	0.277	0.307	0.330	0.256	0.241	0.294	0.269	0.241

[a] Lines: L1, L6, L16 and L61 = control lines; L2, L4, L5 and L45 = selection lines.

Table 7. **Average individual weaning age (day) by line for each generation**

Generations	Lines[a]							
	L1	**L2**	**L4**	**L5**	**L6**	**L45**	**L16**	**L61**
-1	28.656	28.590	~	~	~	~	~	~
0	28.025	27.658	~	~	~	~	~	~
1	27.766	28.428	~	~	~	~	~	~
2	27.018	27.472	~	~	~	~	~	~
3	28.284	28.787	~	~	~	~	~	~
4	27.565	27.245	~	~	~	~	~	~
5	27.488	27.134	~	~	~	~	~	~
6	27.564	27.875	~	~	~	~	~	~
7	27.112	27.311	~	~	~	~	~	~
8	26.125	26.801	~	~	~	~	~	~
9	27.635	27.777	28.847	27.840	27.821	~	~	~
10	27.971	27.815	27.951	27.807	27.396	~	~	~
11	27.539	27.726	27.696	27.795	27.349	~	~	~
12	26.579	27.570	22.229	21.741	22.310	~	~	~
13	9.603	9.713	9.552	9.870	9.628	~	~	~
14	12.204	12.302	12.569	12.656	12.083	~	~	~
15	13.238	13.380	11.836	11.590	11.822	~	~	~
16	11.000	10.811	11.867	11.776	11.120	~	~	~
17	11.697	11.754	11.674	11.387	11.750	~	~	~
18	11.425	11.556	11.846	11.819	11.772	~	~	~
19	12.540	12.451	12.300	12.065	12.175	~	~	~
20	12.201	12.224	~	~	12.370	12.154	~	~
21	11.926	12.176	~	~	12.013	12.064	12.158	~
22	12.071	12.460	~	~	~	12.313	12.394	12.180
23	~	17.541	~	~	~	16.918	17.302	16.312
24	~	18.466	~	~	~	18.862	17.988	16.032
25	~	17.297	~	~	~	16.652	16.861	16.602
26	~	16.743	~	~	~	17.790	17.307	17.495
27	~	17.904	~	~	~	16.354	17.676	16.201
28	~	18.364	~	~	~	~	17.374	~

[a] Lines:

L1, L6, L16 and L61 = control lines; L2, L4, L5 and L45 = selection lines.

Table 8. **Average litter weaning age (day) weaned by line for each generation**

Generations	Lines[a]							
	L1	**L2**	**L4**	**L5**	**L6**	**L45**	**L16**	**L61**
-1	27.877	27.690	~	~	~	~	~	~
0	27.634	28.279	~	~	~	~	~	~
1	27.051	27.349	~	~	~	~	~	~
2	28.167	28.591	~	~	~	~	~	~
3	27.439	27.227	~	~	~	~	~	~
4	27.209	27.205	~	~	~	~	~	~
5	27.780	27.681	~	~	~	~	~	~
6	27.140	27.159	~	~	~	~	~	~
7	26.333	26.523	~	~	~	~	~	~
8	27.368	27.816	~	~	~	~	~	~
9	27.667	27.696	27.857	27.632	27.250	~	~	~
10	27.487	27.623	27.596	27.769	26.973	~	~	~
11	26.756	27.298	22.209	21.773	22.528	~	~	~
12	9.659	9.740	9.500	9.952	10.136	~	~	~
13	12.156	12.200	12.537	12.463	11.974	~	~	~
14	13.025	13.284	11.804	11.568	11.706	~	~	~
15	10.915	10.964	11.738	11.674	11.083	~	~	~
16	11.519	11.678	11.780	11.429	11.581	~	~	~
17	11.394	11.475	11.800	11.792	11.707	~	~	~
18	12.345	12.327	12.133	11.955	12.103	~	~	~
19	12.105	12.170	12.263	12.111	12.361	~	~	~
20	12.012	12.048	~	~	12.022	11.977	~	~
21	12.029	12.316	~	~	12.068	12.269	12.349	~
22	20.000	17.461	~	~	~	16.733	17.316	16.220
23	~	18.492	~	~	~	19.235	17.774	16.057
24	~	17.211	~	~	~	16.553	16.844	16.568
25	~	16.825	~	~	~	17.649	17.227	17.378
26	~	17.871	~	~	~	16.257	17.625	16.220
27	~	18.541	~	~	~	~	17.372	~

[a] Lines:

L1, L6, L16 and L61 = control lines; L2, L4, L5 and L45 = selection lines.

Table 9. **Statistical models used to obtain REML estimates of genetic parameters for each trait[a]**

	Fixed Factors[b]					Random Factors[c]				
Traits[d]	**ctg**	**sex**	**age**	**nns**	**wt**	**a**	**m**	**lit**	**pen**	**e**
BA	√	~	~	~	~	√	~	√	~	√
OR	√	~	~	~	~	√	~	√	~	√
ES	√	~	~	~	~	√	~	√	~	√
SV	√	~	~	~	~	√	~	√	~	√
AP	√	~	~	~	~	√	~	√	~	√
FF	√	~	~	~	~	√	~	√	~	√
MUM	√	~	~	~	~	√	~	√	~	√
SB	√	~	~	~	~	√	~	√	~	√
LBW	√	~	~	~	~	√	~	√	~	√
LWW	√	~	(Q)	(Q)	~	√	~	√	~	√
NW	√	~	(Q)	(Q)	~	√	~	√	~	√
BW	√	√	~	~	~	√	√	√	~	√
WW	√	√	(Q)	~	~	√	√	√	~	√
WT	√	√	(L)	~	~	√	√	√	√	√
BF(age)	√	√	(L)	~	~	√	~	√	√	√
ABF(age)	√	√	(L)	~	~	√	~	√	√	√
LMA(age)	√	√	(L)	~	~	√	~	√	√	√
BF(WT)	√	√	~	~	(L)	√	~	√	√	√
ABF(WT)	√	√	~	~	(L)	√	~	√	√	√
LMA(WT)	√	√	~	~	(L)	√	~	√	√	√
LMA(WT&M)	√	√	~	~	(L)	√	√	√	√	√

[a] " √ " indicates included; " ~ " indicates not included; " (L) " indicates included linear regression coefficient on a covariate; " (Q) " indicates included quadratic regression coefficient on a covariate.

[b] Fixed factors: ctg = contemporary group; sex = gender; age = covariate for age; nns = covariate for number of pigs nursed; wt = covariate for final weight.

[c] Uncorrelated random factors: a = direct additive genetic effects; m = maternal genetic effects; lit = litter effects; pen= pen-mates effects; e = independent residual environmental effects.

[d] Traits: BA = number of pigs born alive; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; FF = number of fully formed pigs; MUM = number of mummified pigs; SB = number of stillborn pigs; LBW = litter birth weight; LWW = litter weaning weight at 28 days for G 0-11, at 12 days for G 12-21 or at 18 days for G 22-27; NW = number of pigs weaned at 28 days for G 0-11, at 12 days for G 12-21 or at 18 days for G 22-27; BW = birth weight; WW = weaning weight at 28 days for G 0-12, at 12 days for G 13-22 or at 18 days for G 23-28; WT = final weight at 180 days; BF(age) or BF(WT) = backfat depth of the 10^{th} rib at age of WT included a covariate of age or a covariate of WT; ABF(age) or ABF(WT) = average backfat depth at age of WT included a covariate of age or a covariate of WT; LMA(age), LMA(WT) or LMA(WT&M) = longissimus muscle area at age of WT included a covariate of age, a covariate of WT or a covariate of WT and a random maternal genetic effect.

Table 10. **Test of significance of linear and/or quadratic regression coefficients for covariates of age and number of pigs nursed and inbreeding coefficients for traits**

	Covariates				
	AGE		Number of Pigs Nursed		Inbreeding
Trait[a]	(Linear)	(Quadratic)	(Linear)	(Quadratic)	(Linear)
BA					-5.99±1.70**
OR					-4.90±3.57
ES					-8.34±3.09**
SV					-0.44±0.20*
AP					50.85±17.80**
FF					-5.64±1.77**
MUM					-1.18±0.59*
SB					0.46±1.01
LBW					-5.50±1.86**
LWW(28d)	1.24±0.15**	-0.13±0.03**	3.43±0.13**	-0.24±0.03**	-7.18±12.16
LWW(12d)	1.36±0.11**	0.01±0.05	1.54±0.05**	-0.04±0.01**	-1.40±4.45
LWW(18d)	1.64±0.20**	0.00±0.03	1.69±0.13**	-0.16±0.02**	-10.44±14.04
NW(28d)	-0.00±0.02	-0.01±0.00*	0.70±0.02**	-0.04±0.00**	0.35±1.59
NW(12d)	-0.09±0.03**	0.05±0.01**	0.71±0.01**	-0.02±0.00**	-0.28±1.12
NW(18d)	-0.03±0.04	-0.01±0.01	0.59±0.02**	-0.04±0.00**	-2.94±2.61
BW					-0.22±0.09*
WW(28d)	0.16±0.01**	-0.01±0.00**			-0.05±0.86
WW(12d)	0.17±0.01**	0.00±0.00			-0.30±0.28
WW(18d)	0.19±0.01**	0.01±0.00**			-0.81±0.75
WT	0.38±0.01**				-30.04±4.42**
BF(age)	0.01±0.00**				-0.55±0.24*
ABF(age)	0.00±0.00**				-0.56±0.24*
LMA(age)	0.08±0.01**				-7.40±1.99**

	Final Weight		
	(Linear)	(Quadratic)	
BF(WT)	0.02±0.00*		0.13±0.20
ABF(WT)	0.02±0.00**		-0.07±0.20
LMA(WT)	0.20±0.00**		-0.99±1.64
LMA(WT&M)	0.20±0.00**		-1.31±1.65

[a] Traits: BA, FF, MUM or SB = number of pigs born alive, fully formed, mummified or stillborn pigs; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; LBW = litter birth weight; LWW(28d), LWW(12d) or LWW(18d) = litter weaning weight at 28, 12 or 18 d; NW(28d), NW(12d) or NW(18d) = number of pigs weaned at 28, 12 or 18 d; BW = birth weight; WW(28d), WW(12d) or WW(18d) = weaning weight at 28, 12 or 18 d; WT = final weight at 180 d; BF(age) or BF(WT) = backfat of the 10th rib with a covariate of age or of WT; ABF(age) or ABF(WT) = average backfat with a covariate of age or WT; LMA(age), LMA(WT) or LMA(WT&M) = longissimus muscle area with a covariate of age, of WT or of WT and a random maternal genetic effect.

[b] t critical values:

* = $P < 0.05$ ($t_{0.05} = 1.96$); ** = $P < 0.01$ ($t_{0.01} = 2.576$).

***Table 11*. Comparison of –2 logLikelihooh at convergence for the model with maternal genetic effects and without maternal genetic effects and tests of significance of differences in –2 logL between the model with maternal genetic effects and without maternal genetic effects**

	-2 logLikelihooh		
Traits[a]	**Without Maternal Genetic Effects**	**With Maternal Genetic Effects**	**Differences Between Two Models**
BW	-99356.121	-99606.000	249.879**
LBW	18008.355	18007.558	0.797
WW(28d)	17751.884	17708.067	43.817**
WW(12d)	-191.019	-275.474	84.455**
WW(18d)	5628.341	5623.616	4.725
LWW(28d)	8817.223	8816.862	0.361
LWW(12d)	12342.928	12342.935	-0.007
LWW(18d)	4715.218	4715.229	-0.011
NW(28d)	2550.999	2550.449	0.550
NW(12d)	5791.167	5792.109	-0.942
NW(18d)	1903.138	1902.977	0.160
WT	77462.625	77442.220	20.405**
ABF(age)	-7971.564	-7975.983	4.419
BF(age)	-4319.181	-4319.496	0.315
LMA(age)	20750.711	20749.909	0.802
ABF(WT)	-10848.420	-10849.114	0.694
BF(WT)	-6252.291	-6252.467	0.176
LMA(WT)	18379.159	18373.205	5.954

[a] Traits:

BW = birth weight; LBW = litter birth weight; WW(28d) = weaning weight at 28 days for generations 0-12; WW(12d) = weaning weight at 12 days for generations 13-22; WW(18d) = weaning weight at 18 days for generations 23-28; LWW(28d) = litter weaning weight at 28 days for generations 0-11; LWW(12d) = litter weaning weight at 12 days for generations 12-21; LWW(18d) = litter weaning weight at 18 days for generations 22-27; NW(28d) = number of weaning pigs at 28 days for generations 0-11; NW(12d) = number of weaning pigs at 12 days for generations 12-21; NW(18d) = number of weaning pigs at 18 days for generations 22-27; WT = final weight at 180 days; ABF(age) = average backfat depth at age of final weight included a fixed covariate of age; ABF(WT) = average backfat depth at age of final weight included a fixed covariate of final weight; BF(age) = backfat depth of the 10^{th} rib at age of final weight included a fixed covariate of age; BF(WT) = backfat depth of the 10^{th} rib at age of final weight included a fixed covariate of final weight; LMA(age) = longissimus muscle area at age of final weight included a fixed covariate of age; LMA(WT) = longissimus muscle area at age of final weight included a fixed covariate of final weight.

[b] Chi-square critical values:

* = $P < 0.05$ ($X^2_{2, 0.05} = 5.991$); ** = $P < 0.01$ ($X^2_{2, 0.01} = 9.210$).

Table 12. **Realized cumulative selection differentials for ovulation rate (OR), number of embryos survived (ES) and embryo survival rate (SV) by line[a] and generation**

Generation	OR				ES		SV	
	LC	L2	L4	L5	LC	L2	LC	L2
0	~	0	~	~	~	0	~	0
1	0	1.095	~	~	0	1.126	0	0.015
2	-0.355	2.890	~	~	-0.010	2.468	0.019	0.018
3	-0.655	4.918	~	~	-0.081	3.627	0.026	0.005
4	-0.408	6.965	~	~	-0.345	5.330	0.001	0.016
5	-0.356	8.879	~	~	0.206	6.946	0.038	0.029
6	-0.266	10.397	~	~	-0.141	8.195	0.008	0.042
7	-0.819	12.271	~	~	0.361	9.897	0.103	0.064
8	-0.891	14.377	~	~	0.363	11.655	0.112	0.077
9	-0.599	17.217	17.217	-0.599	0.588	13.154	0.164	0.070
10	-0.465	20.570	18.751	-0.029	0.564	15.052	0.138	0.071
11	-0.766	24.613	19.015	0.478	0.333	15.895	0.161	0.069
12	~	~	20.096	0.999	~	~	~	~
13	-0.484	~	20.243	1.004	~	~	~	~
14	-0.452	~	20.973	1.604	~	~	~	~
15	-0.014	~	21.663	2.105	~	~	~	~
16	-0.139	~	22.441	2.791	~	~	~	~

[a] Lines:

LC was a control line in generation 0-16;

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11;

L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16.

Table 13. **Realized cumulative selection differentials for number of fully formed pigs by line[a] and generation**

Generation	LC	L2	L4	L5	L45
-1	0	0	~	~	~
0	-0.208	0.125	~	~	~
1	-0.224	0.502	~	~	~
2	-0.328	0.976	~	~	~
3	-0.441	1.180	~	~	~
4	-0.319	1.948	~	~	~
5	0.036	2.421	~	~	~
6	-0.001	2.365	~	~	~
7	0.462	2.846	~	~	~
8	0.542	3.778	~	~	~
9	0.882	4.330	4.330	0.882	~
10	1.177	4.787	5.615	2.162	~
11	1.018	4.416	7.122	3.827	~
12	1.211	5.887	9.143	4.666	~
13	1.321	7.653	10.953	5.892	~
14	1.498	9.283	11.866	7.101	~
15	1.493	10.837	13.271	8.225	~
16	1.578	12.347	14.787	9.472	~
17	2.180	13.067	16.819	11.406	~
18	2.529	14.623	18.472	12.948	~
19	2.300	15.449	19.554	13.726	~
20	2.551	16.870	20.475	14.479	17.477
21	2.672	18.462	~	~	19.039
22	2.728	19.133	~	~	19.642
23	2.863	20.308	~	~	21.217
24	3.069	21.740	~	~	22.960
25	3.459	23.206	~	~	24.555
26	3.700	25.112	~	~	24.373
27	3.460	25.850	~	~	~

[a] Lines: LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17-19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

Table 14. **Realized cumulative selection differentials for number of pigs born alive by line[a] and generation**

Generation	LC	L2	L4	L5	L45
-1	0	0	~	~	~
0	-0.244	0.107	~	~	~
1	-0.214	0.519	~	~	~
2	-0.328	0.837	~	~	~
3	-0.387	1.064	~	~	~
4	-0.307	1.507	~	~	~
5	-0.005	2.191	~	~	~
6	-0.006	2.532	~	~	~
7	0.464	3.015	~	~	~
8	0.328	3.896	~	~	~
9	0.763	4.340	4.340	0.763	~
10	1.036	4.806	5.623	2.058	~
11	0.993	4.464	7.145	3.847	~
12	1.098	6.013	8.295	4.360	~
13	1.219	7.257	9.621	5.598	~
14	1.457	8.674	10.489	6.573	~
15	1.490	10.117	12.225	7.592	~
16	1.588	11.664	13.612	8.845	~
17	2.236	12.326	15.469	10.832	~
18	2.536	13.818	17.090	12.461	~
19	2.328	14.783	18.684	13.924	~
20	2.602	16.673	19.874	14.811	17.342
21	2.577	18.219	~	~	19.192
22	3.050	19.406	~	~	20.355
23	3.308	20.617	~	~	22.212
24	3.672	22.599	~	~	23.472
25	3.890	24.220	~	~	24.928
26	4.024	25.708	~	~	25.211
27	3.843	26.617	~	~	~

[a] Lines: LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17-19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

Table 15. **Realized cumulative selection differentials for birth weight by line[a] and generation**

Generation	LC	L2	L4	L5	L45
-1	0	0	~	~	~
0	-0.036	0.070	~	~	~
1	0.041	0.053	~	~	~
2	0.087	0.134	~	~	~
3	0.176	0.196	~	~	~
4	0.220	0.191	~	~	~
5	0.254	0.282	~	~	~
6	0.370	0.393	~	~	~
7	0.444	0.422	~	~	~
8	0.411	0.427	~	~	~
9	0.476	0.550	0.550	0.476	~
10	0.512	0.576	0.538	0.484	~
11	0.547	0.670	0.570	0.450	~
12	0.597	0.697	0.646	0.463	~
13	0.627	0.694	0.756	0.468	~
14	0.722	0.698	0.832	0.550	~
15	0.758	0.719	0.900	0.564	~
16	0.793	0.756	1.002	0.575	~
17	0.854	0.770	1.103	0.610	~
18	0.936	0.841	1.238	0.710	~
19	1.051	0.979	1.403	0.855	~
20	1.089	1.128	1.589	1.026	1.308
21	1.187	1.262	~	~	1.447
22	1.276	1.315	~	~	1.547
23	1.351	1.446	~	~	1.746
24	1.419	1.535	~	~	1.904
25	1.510	1.672	~	~	2.018
26	1.575	1.765	~	~	2.167
27	1.617	1.885	~	~	2.293

[a] Lines: LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17-19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

Table 16. **Realized cumulative selection differentials for weight at approximately 180 d of age by line[a] and generation**

Generation	LC	L2	L4	L5	L45
-1	0	0	~	~	~
0	0.447	0.200	~	~	~
1	0.699	0.202	~	~	~
2	2.787	-3.049	~	~	~
3	3.297	-2.252	~	~	~
4	0.752	-4.966	~	~	~
5	-0.753	-8.808	~	~	~
6	-3.366	-9.194	~	~	~
7	-1.838	-10.794	~	~	~
8	-2.326	-13.807	~	~	~
9	-3.084	-16.084	-16.084	-3.084	~
10	-1.599	-20.072	-14.019	-0.139	~
11	-0.273	-22.713	-13.008	2.537	~
12	0.095	-22.746	-8.266	6.367	~
13	0.808	-21.751	-4.642	8.273	~
14	2.117	-19.988	-3.430	10.305	~
15	2.963	-20.182	-3.863	12.496	~
16	2.935	-16.555	-3.613	14.662	~
17	4.012	-16.717	-1.759	16.389	~
18	6.879	-12.628	-0.363	18.411	~
19	8.006	-12.026	-0.624	18.422	~
20	7.279	-9.491	0.026	18.763	9.394
21	8.653	-5.697	~	~	13.586
22	10.515	-1.344	~	~	21.339
23	12.437	1.332	~	~	31.365
24	13.711	8.526	~	~	35.175
25	15.419	12.536	~	~	40.685
26	17.687	23.191	~	~	50.600
27	16.819	33.678	~	~	61.170

[a] Lines: LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17-19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

Table 17. **Realized cumulative selection differentials for backfat depth of the 10th rib and longissimus muscle area at age of final weight by line[a] and generation**

	Backfat Depth Of The 10th Rib				
Generation	**LC**	**L2**	**L4**	**L5**	**L45**
18	0	0	0	0	~
19	-0.001	-0.007	-0.058	-0.042	~
20	-0.034	0.021	-0.080	-0.099	-0.090
21	-0.045	0.085	~	~	-0.253
22	-0.037	-0.005	~	~	-0.369
23	0.021	-0.191	~	~	-0.475
24	0.040	-0.109	~	~	-0.731
25	0.002	-0.352	~	~	-0.943
26	0.034	-0.402	~	~	-0.965
27	0.046	-0.325	~	~	-0.942

	Longissimus Muscle Area				
Generation	**LC**	**L2**	**L4**	**L5**	**L45**
18	0	0	0	0	~
19	-0.321	-0.731	-0.206	0.684	~
20	-0.523	-0.125	0.234	0.338	0.286
21	0.062	0.784	~	~	1.234
22	-0.342	2.347	~	~	3.250
23	-0.138	3.139	~	~	5.921
24	-0.324	6.033	~	~	6.550
25	0.091	7.842	~	~	8.066
26	0.576	10.063	~	~	10.140
27	-0.091	12.640	~	~	11.541

[a] Lines: LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17-19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

Table 18. **REML estimates of phenotypic variance (σ_p^2) and fractions due to litter (lit^2), pen-mates (pen^2) and residual (e^2) effects; direct (h_a^2) and maternal (h_m^2) heritability, and direct-maternal genetic correlation (r_{am}) for trait[a]**

Trait	σ_p^2	h_a^2	SE	h_m^2	SE	r_{am}	lit^2	pen^2	e^2
BA	9.39	0.20	0.03				0.02		0.78
OR	19.11	0.27	0.04				0.06		0.67
ES	8.43	0.17	0.04				0.03		0.80
SV	0.04	0.11	0.04				0.02		0.87
AP	710.82	0.57	0.04				0.05		0.38
FF	10.22	0.20	0.03				0.02		0.78
MUM	0.88	0.17	0.03				0.00[b]		0.83
SB	3.17	0.14	0.03				0.07		0.79
LBW	11.42	0.34	0.03				0.00[b]		0.65
LWW (28 d)	97.02	0.21	0.05				0.00[b]		0.79
LWW (12 d)	39.91	0.21	0.04				0.00[b]		0.79
LWW (18 d)	85.78	0.27	0.04				0.00[b]		0.73
NW (28 d)	1.70	0.11	0.04				0.01		0.88
NW (12 d)	3.03	0.13	0.03				0.06		0.81
NW (18 d)	3.10	0.23	0.07				0.00[b]		0.77
BW	0.08	0.06	0.02	0.16	0.02	0.13	0.17		0.60
WW (28 d)	1.60	0.05	0.03	0.12	0.03	-0.06	0.22		0.62
WW (12 d)	0.47	0.01	0.02	0.11	0.02	0.98	0.23		0.63
WW (18 d)	0.99	0.06	0.05	0.07	0.04	0.00	0.24		0.63
WT	131.77	0.36	0.03	0.05	0.02	0.14	0.06	0.01	0.51
BF (age)	0.23	0.51	0.03				0.04	0.01	0.44
ABF (age)	0.17	0.39	0.03				0.10	0.08	0.42
LMA (age)	15.25	0.28	0.03				0.06	0.03	0.63
BF (WT)	0.16	0.47	0.03				0.04	0.01	0.48
ABF (WT)	0.12	0.35	0.03				0.11	0.13	0.41
LMA (WT)	10.77	0.35	0.03				0.05	0.05	0.55
LMA (WT&M)	10.85	0.44	0.05	0.02	0.02	-0.74	0.04	0.05	0.51

[a] Traits: BA, FF, MUM or SB = number of pigs born alive, fully formed pigs, mummified pigs or stillborn pigs; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; LBW = litter birth weight; LWW(28d), LWW(12d) or LWW(18d) = litter weaning weight at 28, 12 or 18 d; NW(28d), NW(12d) or NW(18d) = number of pigs weaned at 28, 12 or 18 d; BW = birth weight; WW(28d), WW(12d) or WW(18d) = weaning weight at 28, 12 or 18 d; WT = final weight at 180 d; BF(age) or BF(WT) = backfat of the 10th rib with a covariate of age or of final weight; ABF(age) or ABF(WT) = average backfat with a covariate of age or final weight; LMA(age), LMA(WT) or LMA(WT&M) = longissimus muscle area with a fixed covariate of age, of final weight or of final weight and a random maternal genetic effect. [b] lit^2_{MUM}= 0.0000012; lit^2_{LBW}= 0.0037; $lit^2_{LWW(28d)}$ = 0.00000001; $lit^2_{LWW(12d)}$ = 0.000000041; $lit^2_{LWW(18d)}$ = 0.000000011; $lit^2_{NW(18d)}$ = 0.000021.

Table 19.1. **Genetic (upper diagonal) and phenotypic (lower diagonal) correlations[a] between traits**

Traits[b]	BA	OR	ES	SV	AP	FF	MUM	SB	LBW	LWW (28d)	LWW (12d)	LWW (18d)	NW (28d)	NW (12d)	NW (18d)
BA		-0.05	0.49	0.30	0.03	0.89	-0.10	-0.07	0.68	0.15	-0.40	-0.15	0.27	-0.46	-0.06
OR	-0.08		0.32	-0.81	-0.18	0.09	0.09	0.53	-0.10	-0.23	-0.18	~	-0.41	-0.41	~
ES	0.51	0.13		0.02	-0.11	0.74	0.17	0.69	0.45	0.08	~	~	0.003	~	~
SV	0.36	-0.40	0.65		0.17	0.13	-0.07	-0.41	0.39	0.36	~	~	0.93	~	~
AP	0.02	-0.07	-0.004	0.10		0.09	-0.03	-0.17	0.10	0.05	-0.38	~	-0.11	-0.18	~
FF	0.84	-0.06	0.67	0.31	-0.02		-0.06	0.39	0.82	0.15	-0.42	-0.06	0.04	-0.53	-0.17
MUM	-0.13	0.05	0.15	0.04	-0.05	-0.09		0.11	-0.14	0.003	-0.23	0.05	-0.24	-0.23	-0.20
SB	-0.21	0.04	0.24	0.13	-0.04	0.35	0.05		0.41	0.01	-0.25	0.17	-0.20	-0.34	-0.04
LBW	0.76	-0.14	0.45	0.39	-0.03	0.83	-0.15	0.21		0.55	0.32	0.49	0.34	-0.15	0.19
LWW(28d)	-0.13	-0.08	-0.09	-0.002	0.07	-0.18	0.01	-0.12	0.17		~	~	0.57	~	~
LWW(12d)	-0.28	-0.14	~	~	-0.06	-0.36	-0.07	-0.22	0.16	~		~	~	0.80	~
LWW(18d)	-0.05	~	~	~	~	-0.28	0.001	-0.20	0.22	~	~		~	~	0.87
NW(28d)	0.03	-0.13	-0.003	0.10	0.03	-0.03	-0.01	-0.11	0.14	0.74	~	~		~	~
NW(12d)	-0.20	-0.24	~	~	-0.04	-0.27	-0.04	-0.19	-0.01	~	0.83	~	~		~
NW(18d)	-0.01	~	~	~	~	-0.17	-0.03	-0.17	0.12	~	~	0.84	~	~	

[a] " ~ " indicates no records for either one trait or both traits.

[b] Traits: BA = number of pigs born alive; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; FF = number of fully formed pigs; MUM = number of mummified pigs; SB = number of stillborn pigs; LBW = litter birth weight; LWW(28d) = litter weaning weight at 28 days in generations 0-11; LWW(12d) = litter weaning weight at 12 days in generations 12-21; LWW(18d) = litter weaning weight at 18 days in generations 22-27; NW(28d) = number of weaning pigs at 28 days in generations 0-11; NW(12d) = number of weaning pigs at 12 days in generations 12-21; NW(18d) = number of weaning pigs at 18 days in generations 22-27.

Table 19.2. **Genetic (upper diagonal) and phenotypic (lower diagonal) correlations[a] between traits**

Traits[b]	BW	WW (28d)	WW (12d)	WW (18d)	WT	BF (age)	ABF (age)	LMA (age)	BF (WT)	ABF (WT)	LMA (WT)	LMA (WT&M)
BW		0.34	0.97	0.91	0.27	0.22	-0.07	0.05	0.08	-0.18	-0.20	-0.25
WW(28d)	0.51		~	~	0.46	~	-0.08	~	~	-0.15	~	~
WW(12d)	0.68	~		~	0.24	0.24	0.26	0.11	-0.12	0.26	-0.51	-0.58
WW(18d)	0.61	~	~		0.42	0.18	~	0.01	-0.11	~	0.23	0.15
WT	0.33	0.41	0.35	0.39		0.60	0.83	0.53	~	~	~	~
BF10(age)	0.09	~	0.10	0.12	0.55		~	0.08	~	~	-0.39	-0.30
ABF(age)	0.05	0.15	0.07	~	0.53	~		~	~	~	~	~
LMA(age)	0.19	~	0.18	0.01	0.56	0.24	~		-0.15	~	~	~
BF10(WT)	-0.10	~	-0.11	-0.12	~	~	~	-0.06		~	-0.23	-0.17
ABF(WT)	-0.12	0.13	0.09	~	~	~	~	~	~		~	~
LMA(WT)	-0.003	~	-0.05	-0.004	~	-0.12	~	~	-0.08	~		~
LMA(WT&M)	0.0002	~	-0.05	-0.002	~	-0.11	~	~	-0.08	~	~	

[a] " ~ " indicates no records for either one trait or both traits.

[b] Traits: BW = birth weight; WW(28d) = weaning weight at 28 days in generations 0-12; WW(12d) = weaning weight at 12 days in generations 13-22; WW(18d) = weaning weight at 18 days in generations 23-28; WT = final weight at 180 days; BF(age) = backfat depth of the 10th rib at age of final weight included a fixed covariate of age; BF(WT) = backfat depth of the 10th rib at age of final weight included a fixed covariate of final weight; ABF(age) = average backfat depth at age of final weight included a fixed covariate of age; ABF(WT) = average backfat depth at age of final weight included a fixed covariate of final weight; LMA(age) = longissimus muscle area at age of final weight included a fixed covariate of age; LMA(WT) = longissimus muscle area at age of final weight included a fixed covariate of final weight; LMA(WT&M) = longissimus muscle area at age of final weight included a fixed covariate of final weight and a random maternal genetic effect.

Table 19.3. **Genetic correlations[a] between traits**

Traits[b]	BA	OR	ES	SV	AP	FF	MUM	SB	LBW	LWW (28d)	LWW (12d)	LWW (18d)	NW (28d)	NW (12d)	NW (18d)
BW	-0.01	0.02	-0.23	-0.31	0.14	-0.03	-0.06	-0.05	0.45	0.37	0.04	0.04	0.54	0.01	0.01
WW(28d)	0.32	0.003	0.14	0.16	0.30	0.41	0.16	0.20	0.53	-0.26	~	~	0.80	~	~
WW(12d)	0.46	-0.16	~	~	-0.95	0.59	0.28	0.43	0.62	~	0.01	~	~	0.11	~
WW(18d)	0.09	~	~	~	~	0.09	0.15	0.25	0.63	~	~	-0.002	~	~	0.45
WT	0.08	-0.01	0.12	0.15	-0.12	0.13	0.08	0.11	0.24	0.19	0.28	0.33	0.10	-0.01	0.13
BF(age)	0.04	~	~	~	~	-0.07	-0.22	-0.20	-0.001	~	0.13	0.34	~	0.23	0.22
ABF(age)	0.04	-0.05	-0.03	0.08	-0.27	-0.02	-0.17	-0.13	-0.08	0.04	0.22	~	0.02	0.20	~
LMA(age)	0.05	~	~	~	~	0.02	0.43	-0.03	0.23	~	0.23	0.28	~	0.16	0.03
BF(WT)	0.10	~	~	~	~	-0.04	-0.41	-0.43	-0.15	~	0.04	0.04	~	0.04	0.19
ABF(WT)	0.09	-0.04	-0.16	-0.03	-0.19	0.01	-0.23	-0.14	-0.22	-0.23	0.07	~	0.03	0.25	~
LMA(WT)	0.05	~	~	~	~	0.03	0.26	-0.11	-0.02	~	0.14	0.14	~	0.15	-0.05
LMA(WT&M)	0.11	~	~	~	~	0.15	0.21	-0.04	-0.02	~	0.10	-0.26	~	0.17	-0.27

[a] " ~ " indicates no records for either one trait or both traits.

[b] Traits: BA = number of pigs born alive; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; FF = number of fully formed pigs; MUM = number of mummified pigs; SB = number of stillborn pigs; LBW = litter birth weight; LWW(28d), LWW(12d) or LWW(18d) = litter weaning weight at 28 days in generations 0-11, at 12 days in generations 12-21 or at 18 days in generations 22-27; NW(28d), NW(12d) or NW(18d) = number of weaning pigs at 28 days in generations 0-11, at 12 days in generations 12-21 or at 18 days in generations 22-27; BW = birth weight; WW(28d), WW(12d) or WW(18d) = weaning weight at 28 days in generations 0-12, at 12 days in generations 13-22 or at 18 days in generations 23-28; WT = final weight at 180 days; BF(age) or BF(WT) = backfat depth of the 10^{th} rib at age of final weight included a fixed covariate of age or a fixed covariate of final weight; ABF(age) or ABF(WT) = average backfat depth at age of final weight included a fixed covariate of age or a fixed covariate of final weight; LMA(age), LMA(WT) or LMA(WT&M) = longissimus muscle area at age of final weight included a fixed covariate of age, a fixed covariate of final weight or a fixed covariate of final weight and a random maternal genetic effect.

Table 19.4. **Phenotypic correlations[a] between traits**

Traits[b]	BA	OR	ES	SV	AP	FF	MUM	SB	LBW	LWW (28d)	LWW (12d)	LWW (18d)	NW (28d)	NW (12d)	NW (18d)
BW	-0.07	0.06	-0.01	-0.06	-0.01	-0.13	-0.02	-0.04	0.11	0.08	0.08	0.09	-0.01	0.04	0.03
WW(28d)	-0.01	0.07	0.03	-0.06	-0.07	-0.02	0.02	-0.02	0.07	0.05	~	~	-0.02	~	~
WW(12d)	-0.05	0.12	~	~	-0.15	-0.08	0.02	-0.01	-0.01	~	0.18	~	~	0.02	~
WW(18d)	-0.06	~	~	~	~	-0.09	0.02	-0.04	0.04	~	~	0.12	~	~	0.05
WT	0.04	0.11	0.08	-0.06	-0.27	0.07	0.05	0.06	0.12	0.08	0.01	0.07	0.01	-0.02	0.01
BF10(age)	0.003	~	~	~	~	-0.01	-0.01	-0.03	-0.01	~	-0.01	0.07	~	0.04	0.04
ABF(age)	0.003	0.04	0.04	-0.01	-0.25	0.01	-0.001	-0.13	-0.02	-0.01	0.01	~	-0.03	-0.004	~
LMA(age)	0.06	~	~	~	~	0.04	0.04	-0.03	0.08	~	0.02	0.08	~	0.002	0.05
BF10(WT)	-0.01	~	~	~	~	-0.04	-0.04	-0.06	-0.08	~	-0.02	0.026	~	0.02	0.03
ABF(WT)	-0.02	-0.02	-0.02	0.02	-0.15	-0.02	-0.03	-0.002	-0.09	-0.10	-0.001	~	-0.05	0.01	~
LMA(WT)	0.04	~	~	~	~	0.01	0.02	-0.06	0.02	~	0.02	0.03	~	0.01	0.05
LMA(WT&M)	0.04	~	~	~	~	0.03	0.02	-0.05	-0.05	~	0.02	0.05	~	0.01	0.05

[a] " ~ " indicates no records for either one trait or both traits.

[b] Traits: BA = number of pigs born alive; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; FF = number of fully formed pigs; MUM = number of mummified pigs; SB = number of stillborn pigs; LBW = litter birth weight; LWW(28d), LWW(12d) or LWW(18d) = litter weaning weight at 28 days in generations 0-11, at 12 days in generations 12-21 or at 18 days in generations 22-27; NW(28d), NW(12d) or NW(18d) = number of weaning pigs at 28 days in generations 0-11, at 12 days in generations 12-21 or at 18 days in generations 22-27; BW = birth weight; WW(28d), WW(12d) or WW(18d) = weaning weight at 28 days in generations 0-12, at 12 days in generations 13-22 or at 18 days in generations 23-28; WT = final weight at 180 days; BF(age) or BF(WT) = backfat depth of the 10^{th} rib at age of final weight included a fixed covariate of age or a fixed covariate of final weight; ABF(age) or ABF(WT) = average backfat depth at age of final weight included a fixed covariate of age or a fixed covariate of final weight; LMA(age), LMA(WT) or LMA(WT&M) = longissimus muscle area at age of final weight included a fixed covariate of age, a fixed covariate of final weight or a fixed covariate of final weight and a random maternal genetic effect.

Table 20. **Coefficients (b) and SE for regression of mean estimated direct and maternal breeding values on generation for selection Line 2 by trait[a]**

	Selection Traits and Selection Generations							
	OR+ES (G 0-11)		FF (G 12-14)		BA+BW (G 15-19)		BA+WT+BF+LMA (G 20-28)	
Trait	**b**	**SE**	**b**	**SE**	**b**	**SE**	**b**	**SE**
	Estimated Breeding Values							
BA	0.052‡	0.007	0.222†	0.006	0.123†	0.025	0.176‡	0.024
OR	0.525‡	0.012						
ES	0.258‡	0.007						
SV	-0.002‡	0.001						
AP	-0.708‡	0.152	0.013	0.869				
FF	0.119‡	0.008	0.195*	0.017	0.120†	0.033	0.165‡	0.037
MUM	0.021‡	0.006	-0.034†	0.002	-0.015†	0.004	0.000	0.003
SB	0.068‡	0.004	-0.027	0.005	-0.001	0.015	-0.011	0.014
LBW	0.031*	0.014	0.165†	0.012	0.103*	0.036	0.311‡	0.043
LWW	-0.206‡	0.036	-0.358†	0.021	-0.088	0.094	0.086	0.134
NW	-0.025‡	0.003	-0.077	0.021	-0.025	0.011	0.017	0.023
BW	-0.002‡	0.000	-0.002	0.001	0.001	0.001	0.004‡	0.001
WW	0.002	0.001	-0.018	0.007	-0.002*	0.001	0.000	0.004
WT	-0.614‡	0.047	-0.228*	0.022	0.535†	0.104	1.814‡	0.243
BF1							-0.006	0.006
ABF1	-0.002†	0.001	-0.012	0.002	-0.006	0.027		
LMA1							0.330‡	0.052
BF2							-0.006	0.006
ABF2	-0.003†	0.001	-0.012	0.002	-0.005	0.025		
LMA2							0.394‡	0.058
LMA3							0.466‡	0.062
	Estimated Maternal Breeding Values							
BW	-0.006‡	0.001	-0.009	0.002	-0.005†	0.001	-0.004‡	0.001
WW	-0.009†	0.003	0.003	0.015	-0.007	0.004	0.014‡	0.002
WT	0.040‡	0.012	-0.016	0.074	0.131†	0.033	0.107	0.081
LMA3							-0.019‡	0.004

[a] Traits: BA, FF, MUM or SB = number of pigs born alive, fully formed pigs, mummified pigs or stillborn pigs; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; LBW = litter birth weight; LWW = litter weaning weight; NW = number of pigs weaned; BW = birth weight; WW = weaning weight; WT = final weight at 180 d of age; BF1 or BF2 = backfat of the 10^{th} rib with a covariate of age or of final weight; ABF1 or ABF2 = average backfat with a covariate of age or final weight; LMA1, LMA2 or LMA3 = longissimus muscle area with a fixed covariate of age, of final weight or of final weight and a random maternal genetic effect. *P $<$ 0.1; †P $<$ 0.05; ‡P $<$ 0.01.

Table 21. **Coefficients (b) and SE for regression of mean estimated direct and maternal breeding values on generation for selection Lines 4, 5 and 45 by trait[a]**

	Selection Traits and Selection Generations									
	OR+LS (G 8-16)				BA+BW (G 17-19)				BA+WT+BF+LMA (G 20-28)	
	Line 4		Line 5		Line 4		Line 5		Line 45	
Trait	**b**	**SE**	**b**	**SE**	**b**	**SE**	**b**	**SE**	**b**	**SE**
	Estimated Breeding Values									
BA	0.186‡	0.018	0.281‡	0.011	0.168	0.029	0.389*	0.058	0.170‡	0.028
OR	0.049	0.031	0.211‡	0.015						
AP	-1.722‡	0.300	-1.623‡	0.149						
FF	0.265‡	0.012	0.292‡	0.011	0.110	0.019	0.464*	0.054	0.171‡	0.030
MUM	-0.019‡	0.005	0.017	0.009	-0.008	0.002	-0.035	0.018	0.020‡	0.004
SB	0.059‡	0.015	0.011†	0.004	-0.038*	0.006	0.048	0.009	-0.003	0.010
LBW	0.394‡	0.028	0.218‡	0.023	0.195	0.047	0.780*	0.104	0.312‡	0.069
LWW	0.047	0.117	-0.496‡	0.132	0.442‡	0.002	-0.204	0.252	0.981‡	0.153
NW	-0.071‡	0.008	0.009	0.005	0.034	0.009	-0.040	0.049	0.075‡	0.009
BW	0.006‡	0.001	-0.004‡	0.000	0.005*	0.001	0.005	0.001	0.005‡	0.001
WW	-0.001	0.001	-0.016‡	0.003	0.002	0.003	-0.002	0.001	0.028‡	0.004
WT	1.065‡	0.122	0.142*	0.066	0.330*	0.045	0.419*	0.060	1.549‡	0.183
BF1									-0.046‡	0.010
ABF1	0.025‡	0.005	0.027‡	0.003						
LMA1									0.405‡	0.028
BF2									-0.043‡	0.009
ABF2	0.024‡	0.005	0.026‡	0.003						
LMA2									0.466‡	0.035
LMA3									0.544‡	0.036
	Estimated Maternal Breeding Values									
BW	0.000	0.002	-0.012‡	0.003	-0.005	0.009	-0.013	0.008	-0.002	0.001
WW	0.026‡	0.006	-0.027*	0.013	0.003	0.005	-0.012	0.009	0.040‡	0.008
WT	0.100†	0.034	-0.027	0.042	-0.047	0.009	0.153	0.097	0.115‡	0.027
LMA3									-0.017†	0.007

[a] Traits: BA, FF, MUM or SB = number of pigs born alive, fully formed pigs, mummified pigs or stillborn pigs; LS = litter size; OR = ovulation rate; AP = age of puberty; LBW = litter birth weight; LWW = litter weaning weight; NW = number of pigs weaned; BW = birth weight; WW = weaning weight; WT = final weight at 180 d of age; BF1 or BF2 = backfat of the 10^{th} rib with a covariate of age or of final weight; ABF1 or ABF2 = average backfat with a covariate of age or final weight; LMA1, LMA2 or LMA3 = longissimus muscle area with a fixed covariate of age, of final weight or of final weight and a random maternal genetic effect. *$P < 0.1$; †$P < 0.05$; ‡$P < 0.01$.

Table 22. **Coefficients (b) and SE for regression of phenotypic means on generation for selection Line 2 by trait[a]**

	Selection Traits and Selection Generations							
	OR+ES (G 0-11)		FF (G 12-14)		BA+BW (G 15-19)		BA+WT+BF+LMA (G 20-28)	
Trait	**b**	**SE**	**b**	**SE**	**b**	**SE**	**b**	**SE**
BA	0.005	0.041	-0.059	0.606	0.114	0.210	0.221	0.130
OR	0.768‡	0.062						
ES	0.294‡	0.026						
SV	-0.010‡	0.002						
AP	-0.413	0.418	-2.250	6.865				
FF	0.126‡	0.033	-0.182	0.189	0.101	0.286	0.181	0.121
MUM	0.059	0.045	-0.061	0.024	0.034	0.030	0.014	0.012
SB	0.121‡	0.025	-0.123	0.418	-0.008	0.232	-0.042	0.172
LBW	-0.145†	0.049	-0.427	0.109	-0.034	0.120	0.204†	0.069
LWW	-0.875‡	0.196	4.565	2.111	1.024	1.159	1.837‡	0.440
NW	-0.048	0.032	0.073	0.103	0.208	0.243	0.094	0.070
BW	-0.026‡	0.003	-0.005	0.019	-0.010	0.008	0.004	0.005
WW	-0.087‡	0.018	-1.461	1.235	-0.038	0.096	0.215‡	0.045
WT	0.382*	0.190	-1.301	1.814	-2.752	1.513	1.276*	0.637
BF							0.013	0.021
ABF	-0.003	0.009	0.022	0.088	0.020	0.338		
LMA							-0.695	0.437

[a] Traits: BA, FF, MUM or SB = number of pigs born alive, fully formed pigs, mummified pigs or stillborn pigs; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; LBW = litter birth weight; LWW = litter weaning weight; NW = number of pigs weaned; BW = birth weight; WW = weaning weight; WT = final weight at 180 d of age; BF = backfat of the 10^{th} rib at 180 d of age; ABF = average backfat at 180 d of age; LMA = longissimus muscle area at 180 d of age. *$P < 0.1$; †$P < 0.05$; ‡$P < 0.01$.

Table 23. **Coefficients (b) and SE for regression of phenotypic means on generation for selection Lines 4, 5 and 45 by trait[a]**

	Selection Traits and Selection Generations									
	OR+LS (G 8-16)				BA+BW (G 17-19)				BA+WT+BF+LMA (G 20-28)	
	Line 4		Line 5		Line 4		Line 5		Line 45	
Trait	**b**	**SE**	**b**	**SE**	**b**	**SE**	**b**	**SE**	**b**	**SE**
BA	0.097	0.100	0.107	0.079	-0.516	0.715	0.346	0.451	0.139	0.143
OR	0.257†	0.073	0.335‡	0.025						
AP	-3.650‡	0.878	-3.553‡	0.566						
FF	0.271†	0.083	0.153	0.100	-0.883	0.722	0.517	0.214	0.032	0.168
MUM	0.089†	0.034	0.095†	0.028	0.005	0.101	-0.048	0.069	0.045†	0.018
SB	0.174	0.122	0.046	0.031	-0.367†	0.007	0.171	0.665	-0.107†	0.038
LBW	0.243	0.133	-0.011	0.103	-0.674	0.786	1.036	0.177	0.061	0.187
LWW	-4.839‡	1.214	-5.084†	1.430	-1.097	0.823	-2.312	0.642	2.253†	0.844
NW	-0.118	0.101	0.022	0.089	-0.565	0.318	-0.403	0.241	0.128	0.108
BW	-0.006	0.008	-0.021‡	0.005	0.005	0.014	-0.009	0.037	0.001	0.003
WW	-0.631‡	0.115	-0.673‡	0.124	0.053†	0.003	-0.010	0.006	0.221†	0.081
WT	0.121	0.592	-1.019†	0.395	2.224	0.852	3.157	0.585	1.248	0.718
BF									-0.013	0.034
ABF	0.090‡	0.022	0.089‡	0.013						
LMA									-0.969†	0.295

[a] Traits: BA, FF, MUM or SB = number of pigs born alive, fully formed pigs, mummified pigs or stillborn pigs; LS = litter size; OR = ovulation rate; AP = age of puberty; LBW = litter birth weight; LWW = litter weaning weight; NW = number of pigs weaned; BW = birth weight; WW = weaning weight; WT = final weight at 180 d of age; BF = backfat of the 10^{th} rib at 180 d of age; ABF = average backfat at 180 d of age; LMA = longissimus muscle area at 180 d of age. *P $<$ 0.1; †P $<$ 0.05; ‡P $<$ 0.01.

Table 24.1. **Coefficients (b) and SE for regression of mean estimated direct breeding values and phenotypic means on generation for control Line C by trait[a]**

	Estimated Breeding Values		Phenotypic Mean	
Trait	**b**	**SE**	**b**	**SE**
BA	0.006*	0.003	-0.032†	0.014
BA (G 0-11)	-0.020†	0.008	-0.070	0.050
BA (G 12-27)	0.025‡	0.004	-0.010	0.035
OR	-0.018	0.018	-0.032	0.051
ES	-0.001	0.016	0.061	0.068
SV	0.003‡	0.000	-0.002	0.004
AP	-0.567‡	0.126	-0.710†	0.250
FF	-0.014‡	0.004	-0.022	0.014
MUM	0.002	0.002	-0.016‡	0.006
MUM (G 0-11)	-0.018†	0.007	-0.011	0.029
MUM (G 12-27)	0.000	0.001	-0.010	0.006
SB	-0.023‡	0.002	0.009*	0.005
SB (G 0-11)	-0.038‡	0.003	0.038†	0.016
SB (G 12-27)	-0.008‡	0.002	0.003	0.010
LBW	0.039‡	0.005	-0.066‡	0.019
LWW	-0.001	0.014	-1.116‡	0.194
LWW (28 d)	0.153‡	0.027	-0.628†	0.260
LWW (12 d)	-0.025*	0.011	0.089	0.245
LWW (18 d)	0.019	0.172	-0.238	0.626
NW	0.022‡	0.001	0.007	0.011
NW (28 d)	0.016‡	0.002	0.017	0.034
NW (12 d)	0.015‡	0.002	-0.029	0.074
NW (18 d)	0.025	0.020	0.091	0.052

[a] Traits: BA, FF, MUM or SB = number of pigs born alive, fully formed pigs, mummified pigs or stillborn pigs for generations 0-27; BA (G 0-11), MUM (G 0-11) or SB (G 0-11) = number of pigs born alive, mummified pigs or stillborn pigs for generations 0-11; BA (G 12-27), MUM (G 12-27) or SB (G 12-27) = number of pigs born alive, mummified pigs or stillborn pigs for generations 12-27; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; LBW = litter birth weight; LWW = litter weaning weight for generations 0-27; NW = number of pigs weaned for generations 0-27; LWW(28d), LWW(12d) or LWW(18d) = litter weaning weight at 28 d for generations 0-11, at 12 d for generations 12-21 or at 18 d for generations 22-27; NW(28d), NW(12d) or NW(18d) = number of pigs weaned at 28 d for generations 0-11, at 12 d for generations 12-21 or at 18 d for generations 22-27. *$P < 0.1$; †$P < 0.05$; ‡$P < 0.01$.

Table 24.2. **Coefficients (b) and SE for regression of mean estimated direct and maternal breeding values and phenotypic means on generation for control Line C by trait[a]**

	Estimated Direct Breeding Values		Estimated Maternal Breeding Values		Phenotypic Mean	
Trait	**b**	**SE**	**b**	**SE**	**b**	**SE**
BW	0.002‡	0.000	0.002‡	0.000	-0.005‡	0.001
BW (G 0-11)	0.004‡	0.000	0.006‡	0.001	-0.005	-0.005
BW (G 12-28)	0.001†	0.000	-0.003‡	0.001	-0.002	0.002
WW	-0.001	0.001	-0.005‡	0.001	-0.140‡	0.022
WW (28 d)	0.004‡	0.001	0.008†	0.003	-0.075‡	0.021
WW (12 d)	-0.001	0.000	-0.002†	0.001	0.023	0.018
WW (18 d)	0.009†	0.003	0.029	0.061	0.029	0.061
WT	0.026	0.025	-0.007	0.004	0.274‡	0.085
WT (G 0-19)	-0.202‡	0.022	-0.023‡	0.004	0.326†	0.129
WT (G 20-27)	0.274‡	0.044	0.067†	0.025	-0.038	0.751
BF	0.014‡	0.003			0.029	0.018
ABF	0.006‡	0.001			0.030‡	0.006
LMA	0.110‡	0.022	-0.004‡	0.001	-0.614*	0.282

[a] BW, WW or WT = birth weight, weaning weight or final weight at 180 d; WW(28d), WW(12d) or WW(18d) = weaning weight at 28 d for generations 0-12, at 12 d for generations 13-22 or at 18 d for generations 23-28; BF(age) or BF(WT) = backfat depth of the 10th rib with a covariate of age or of final weight; ABF(age) or ABF(WT) = average backfat depth with a covariate of age or final weight; LMA(age), LMA(WT) or LMA(WT&M) = longissimus muscle area with a fixed covariate of age, of final weight or of final weight and a random maternal genetic effect. *P $<$ 0.1; †P $<$ 0.05; ‡P $<$ 0.01.

Table 25.1. **Coefficients (b) and SE for regression of difference in mean estimated breeding values on generation between selection lines and control line by trait[a]**

	Differences Between Selection Lines and Control Line							
	L2-LC		L4-LC		L5-LC		L45-LC	
Trait	**b**	**SE**	**b**	**SE**	**b**	**SE**	**b**	**SE**
BA	0.124‡	0.005	0.171‡	0.012	0.290‡	0.009	0.103†	0.027
BA (G 0-11)	0.071‡	0.015						
BA (G 12-27)	0.154‡	0.008						
OR	0.596‡	0.037	-0.023	0.061	0.147‡	0.022		
ES	0.259‡	0.017						
SV	-0.006‡	0.001						
AP	-0.271	0.200	-2.166‡	0.264	-2.066‡	0.226		
FF	0.176‡	0.006	0.221‡	0.023	0.332‡	0.009	0.108†	0.032
MUM	-0.014‡	0.004	-0.021‡	0.005	-0.013†	0.005	0.022‡	0.004
MUM (G 0-11)	0.038‡	0.0124						
MUM (G 12-27)	-0.011‡	0.0021						
SB	0.052‡	0.006	0.048†	0.015	0.041‡	0.002	0.003	0.008
SB (G 0-11)	0.105‡	0.005						
SB (G 12-27)	-0.007	0.005						
LBW	0.139‡	0.012	0.280‡	0.039	0.278‡	0.030	0.181*	0.072
LWW	-0.160‡	0.021	0.142	0.099	-0.144†	0.052	0.987‡	0.152
LWW (28 d)	-0.359‡	0.057	-0.464	0.686	-0.189†	0.013		
LWW (12 d)	-0.132‡	0.039	-0.154	0.080	0.036	0.040		
LWW (18 d)	0.399	0.202					0.899†	0.264
NW	-0.068‡	0.003	-0.091‡	0.008	-0.031‡	0.006	0.025†	0.008
NW (28 d)	-0.047‡	0.004	-0.024	0.041	0.010	0.006		
NW (12 d)	-0.057‡	0.009	-0.090‡	0.015	-0.024†	0.010		
NW (18 d)	0.008	0.028					0.023	0.013

[a] Traits: BA, FF, MUM or SB = number of pigs born alive, fully formed pigs, mummified pigs or stillborn pigs for generations 0-27; BA (G 0-11), MUM (G 0-11) or SB (G 0-11) = number of pigs born alive, mummified pigs or stillborn pigs for generations 0-11; BA (G 12-27), MUM (G 12-27) or SB (G 12-27) = number of pigs born alive, mummified pigs or stillborn pigs for generations 12-27; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; LBW = litter birth weight; LWW = litter weaning weight for generations 0-27; NW = number of pigs weaned for generations 0-27; LWW(28d), LWW(12d) or LWW(18d) = litter weaning weight at 28 d for generations 0-11, at 12 d for generations 12-21 or at 18 d for generations 22-27; NW(28d), NW(12d) or NW(18d) = number of pigs weaned at 28 d for generations 0-11, at 12 d for generations 12-21 or at 18 d for generations 22-27. *$P < 0.1$; †$P < 0.05$; ‡$P < 0.01$.

Table 25.2. **Coefficients (b) and SE for regression of difference in mean estimated direct and maternal breeding values on generation between selection lines and control line by trait[a]**

	Differences Between Selection Lines and Control Line							
	L2-LC		L4-LC		L5-LC		L45-LC	
Trait	**b**	**SE**	**b**	**SE**	**b**	**SE**	**b**	**SE**
	Estimated Breeding Values							
BW	-0.001	0.000	0.005‡	0.001	-0.002‡	0.000	0.001	0.001
BW (G 0-11)	-0.006‡	0.000						
BW (G 12-28)	0.002‡	0.001						
WW	-0.001†	0.001	0.007‡	0.001	-0.004‡	0.001	0.022‡	0.003
WW (28 d)	-0.002	0.001	0.007	0.006	0.003	0.006		
WW (12 d)	-0.001	0.001	0.000	0.001	-0.003‡	0.000	-0.001	0.003
WW (18 d)	0.005	0.005					0.015†	0.004
WT	0.058	0.066	0.665‡	0.123	0.210‡	0.059	1.106‡	0.260
WT (G 0-14)	-0.351‡	0.036						
WT (G 15-27)	0.928‡	0.142						
BF (Age)	-0.015†	0.006					-0.058‡	0.011
ABF (Age)	-0.005‡	0.002	0.023‡	0.005	0.022‡	0.005		
LMA (Age)	0.420†	0.142					0.113	0.222
BF (WT)	-0.010	0.006					-0.053‡	0.011
ABF (WT)	-0.005‡	0.002	0.023‡	0.005	0.022‡	0.005		
LMA (WT)	0.197‡	0.048					0.321‡	0.046
LMA (WT&M)	0.278‡	0.061					0.431‡	0.057
	Estimated Maternal Breeding Values							
BW	-0.003‡	0.001	0.005*	0.003	-0.004	0.002	0.002	0.002
WW	0.001	0.002	0.033‡	0.009	-0.004	0.008	0.044‡	0.007
WW (28 d)	-0.016†	0.005	0.045	0.036	0.083	0.055		
WW (12 d)	-0.005	0.004	-0.008†	0.003	-0.013‡	0.001	0.008	0.011
WW (18 d)	0.013*	0.005					0.021†	0.007
WT	0.069‡	0.008	0.090	0.032	0.074	0.022	0.048	0.040
LMA (WT&M)	-0.007	0.004					-0.013	0.007

[a] BW, WW or WT = birth weight, weaning weight or final weight at 180 d; WW(28d), WW(12d) or WW(18d) = weaning weight at 28 d for generations 0-12, at 12 d for generations 13-22 or at 18 d for generations 23-28; BF(age) or BF(WT) = backfat depth of the 10th rib with a covariate of age or of final weight; ABF(age) or ABF(WT) = average backfat depth with a covariate of age or final weight; LMA(age), LMA(WT) or LMA(WT&M) = longissimus muscle area with a fixed covariate of age, of final weight or of final weight and a random maternal genetic effect. *P $<$ 0.1; †P $<$ 0.05; ‡P $<$ 0.01.

Table 26.1. **Coefficients (b) and SE for regression of difference in estimated phenotypic mean on generation between selection lines and control line by trait[a]**

	Differences Between Selection Lines and Control Line							
	L2-LC		L4-LC		L5-LC		L45-LC	
Trait	**b**	**SE**	**b**	**SE**	**b**	**SE**	**b**	**SE**
BA	0.113‡	0.014	0.141	0.078	0.268‡	0.052	-0.043	0.071
BA (G 0-11)	0.075*	0.041						
BA (G 12-27)	0.102†	0.038						
OR	0.704‡	0.114	0.255†	0.078	0.337‡	0.060		
ES	0.233†	0.076						
SV	-0.008*	0.004						
AP	0.045*	0.260	-2.768	1.102	-2.671†	0.707		
FF	0.163‡	0.018	0.210†	0.074	0.330‡	0.043	-0.072	0.100
MUM	-0.027†	0.010	0.015	0.018	-0.007	0.020	0.047†	0.017
MUM (G 0-11)	0.070*	0.038						
MUM (G 12-27)	-0.002	0.007						
SB	0.050‡	0.014	0.070	0.074	0.062	0.038	-0.016	0.043
SB (G 0-11)	0.083‡	0.025						
SB (G 12-27)	-0.014	0.041						
LBW	0.139‡	0.020	0.202†	0.076	0.204†	0.069	0.013‡	0.130
LWW	-0.081	0.068	-0.133	0.239	-0.126	0.307	0.829	0.905
LWW (28 d)	-0.247	0.274	-2.987*	0.245	-3.821	4.421		
LWW (12 d)	-0.075	0.217	-0.108	0.398	0.279	0.272		
LWW (18 d)	1.253	0.709					1.966	1.751
NW	-0.026*	0.011	-0.083	0.050	0.089†	0.038	-0.048	0.109
NW (28 d)	-0.065†	0.024	0.093	0.234	-0.204	0.219		
NW (12 d)	-0.012	0.072	-0.075	0.096	0.160†	0.057		
NW (18 d)	0.123	0.104					0.210	0.131

[a] Traits: BA, FF, MUM or SB = number of pigs born alive, fully formed pigs, mummified pigs or stillborn pigs for generations 0-27; BA (G 0-11), MUM (G 0-11) or SB (G 0-11) = number of pigs born alive, mummified pigs or stillborn pigs for generations 0-11; BA (G 12-27), MUM (G 12-27) or SB (G 12-27) = number of pigs born alive, mummified pigs or stillborn pigs for generations 12-27; OR = ovulation rate; ES = number of embryos survived; SV = embryo survival rate; AP = age of puberty; LBW = litter birth weight; LWW = litter weaning weight for generations 0-27; NW = number of pigs weaned for generations 0-27; LWW(28d), LWW(12d) or LWW(18d) = litter weaning weight at 28 d for generations 0-11, at 12 d for generations 12-21 or at 18 d for generations 22-27; NW(28d), NW(12d) or NW(18d) = number of pigs weaned at 28 d for generations 0-11, at 12 d for generations 12-21 or at 18 d for generations 22-27. *$P < 0.1$; †$P < 0.05$; ‡$P < 0.01$.

Table 26.2. **Coefficients (b) and SE for regression of difference in estimated phenotypic mean on generation between selection lines and control line by trait[a]**

	Differences Between Selection Lines and Control Line							
	L2-LC		L4-LC		L5-LC		L45-LC	
Trait	**b**	**SE**	**b**	**SE**	**b**	**SE**	**b**	**SE**
BW	-0.002	0.002	0.000	0.002	-0.014‡	0.003	0.005	0.003
BW (G 0-11)	-0.021‡	0.004						
BW (G 12-28)	0.003	0.003						
WW	0.006	0.005	0.012	0.020	-0.020	0.019	0.053	0.044
WW (28 d)	-0.003	0.020	-0.146	0.070	-0.068	0.141		
WW (12 d)	-0.003	0.013	-0.019	0.034	-0.033	0.033	0.134*	0.012
WW (18 d)	0.034	0.047					-0.008	0.121
WT	0.197†	0.092	0.675†	0.267	0.219	0.368	1.286†	0.435
WT (G 0-19)	-0.007	0.012						
WT (G 20-28)	0.039*	0.020						
BF	0.002	0.020					-0.053†	0.021
ABF	-0.009*	0.005	0.033	0.022	0.031*	0.015		
LMA	0.420†	0.142					0.113	0.222

[a] BW, WW or WT = birth weight, weaning weight or final weight at 180 d; WW(28d), WW(12d) or WW(18d) = weaning weight at 28 d for generations 0-12, at 12 d for generations 13-22 or at 18 d for generations 23-28; BF(age) or BF(WT) = backfat depth of the 10^{th} rib with a covariate of age or of final weight; ABF(age) or ABF(WT) = average backfat depth with a covariate of age or final weight; LMA(age), LMA(WT) or LMA(WT&M) = longissimus muscle area with a fixed covariate of age, of final weight or of final weight and a random maternal genetic effect. *$P < 0.1$; †$P < 0.05$; ‡$P < 0.01$.

Table 27. **Significant linear and quadratic regression coefficients for cumulative selection differential on generation, for mean of estimated direct breeding values on generation, and estimates of genetic variance for number of pigs born alive by selection lines and selection traits[a]**

	Selection Traits and Selection Generation			
	OR+ES (G 0-11)	**FF; BA+BW (G 12-19)**	**OR+LS; BA+BW (G 8-19)**	**BA+WT+BF+LMA (G 20-27)**
Line	**Significant Linear and Quadratic Regression Coefficients**			
	Cumulative Selection Differential			
L2	L: 0.438G	L: 1.270G	~	L: 1.470G
L4	~	~	L: 1.425G Q: $0.767G+0.022G^2$	~
L5	~	~	L: 1.275G	~
L45	~	~	~	L: 1.364G
	Direct Breeding Values			
L2	L: 0.052G Q: $0.110G-0.006G^2$	L: 0.150G	~	L: 0.176G
L4	~	~	L: 0.179G	~
L5	~	~	L: 0.298G Q: $0.102G+0.007G^2$	~
L45	~	~	~	L: 0.170G
Line	**Genetic Variance**			
L2	2.182	1.586	~	5.469
L4	~	~	2.336	~
L5	~	~	0.002	~
L45	~	~	~	0.950

[a] t critical values: $P < 0.01$. " L " indicates significant linear regression coefficient; " Q " indicates significant quadratic regression coefficient; " G " indicates generation. Traits: OR = ovulation rate; ES = number of embryos survived; BA = number of pigs born alive; FF = number of fully formed pigs; LS = litter size; BW = birth weight; WT = final weight at 180 d of age; BF = backfat of the 10^{th} rib at 180 d of age; LMA = longissimus muscle area at 180 d of age.

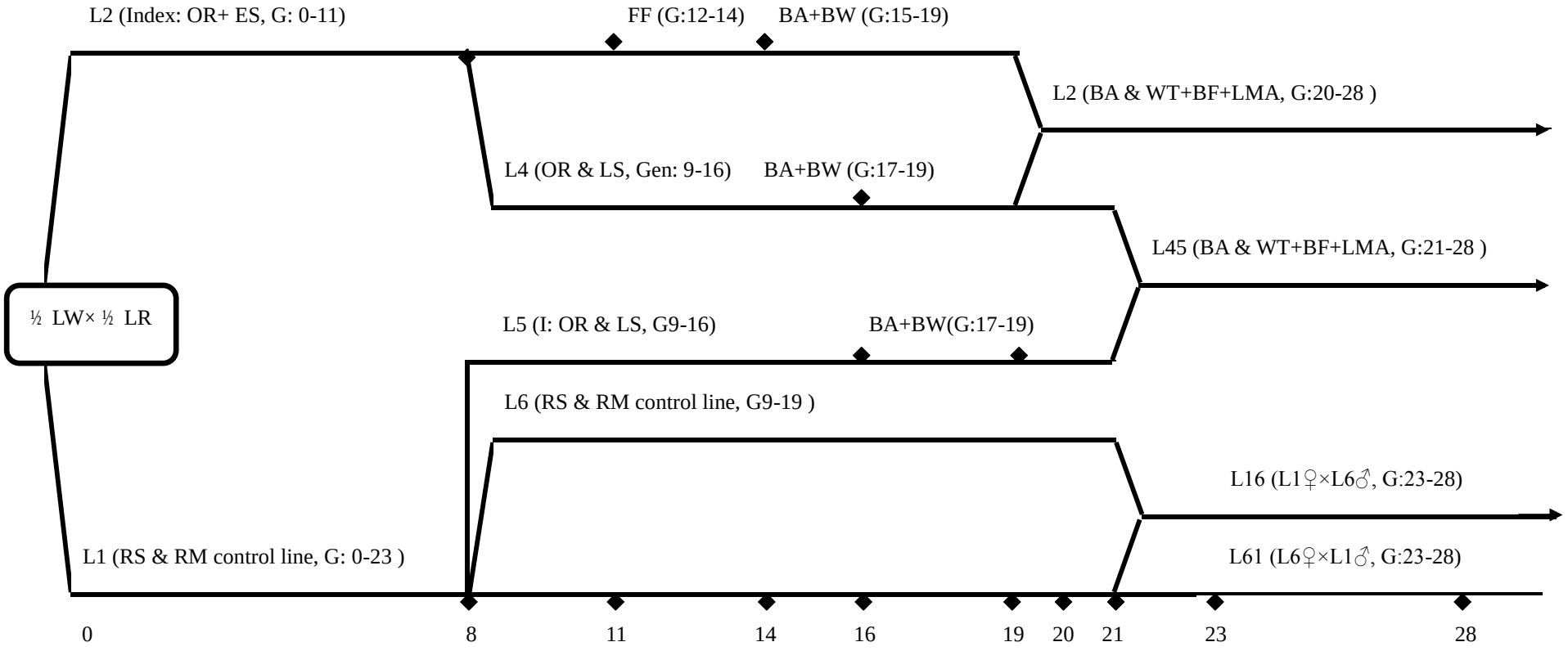

Figure 1. **Description of selected and control lines by generation**[a]

[a] LW = Large White breed; LR = Landrace breed; L1, L6, L16 and L61 = control lines; L2, L4, L5 and L45 = selection lines; G = generations; OR = ovulation rate; ES = number of embryos survived; FF = number of fully formed pigs; BA = number of born alive pigs; BW = birth weight; WT = final weight; BF = backfat at age of final weight; LMA = longissimus muscle area at age of final weight; LS = litter size; RS = random selection; RM = random mating.

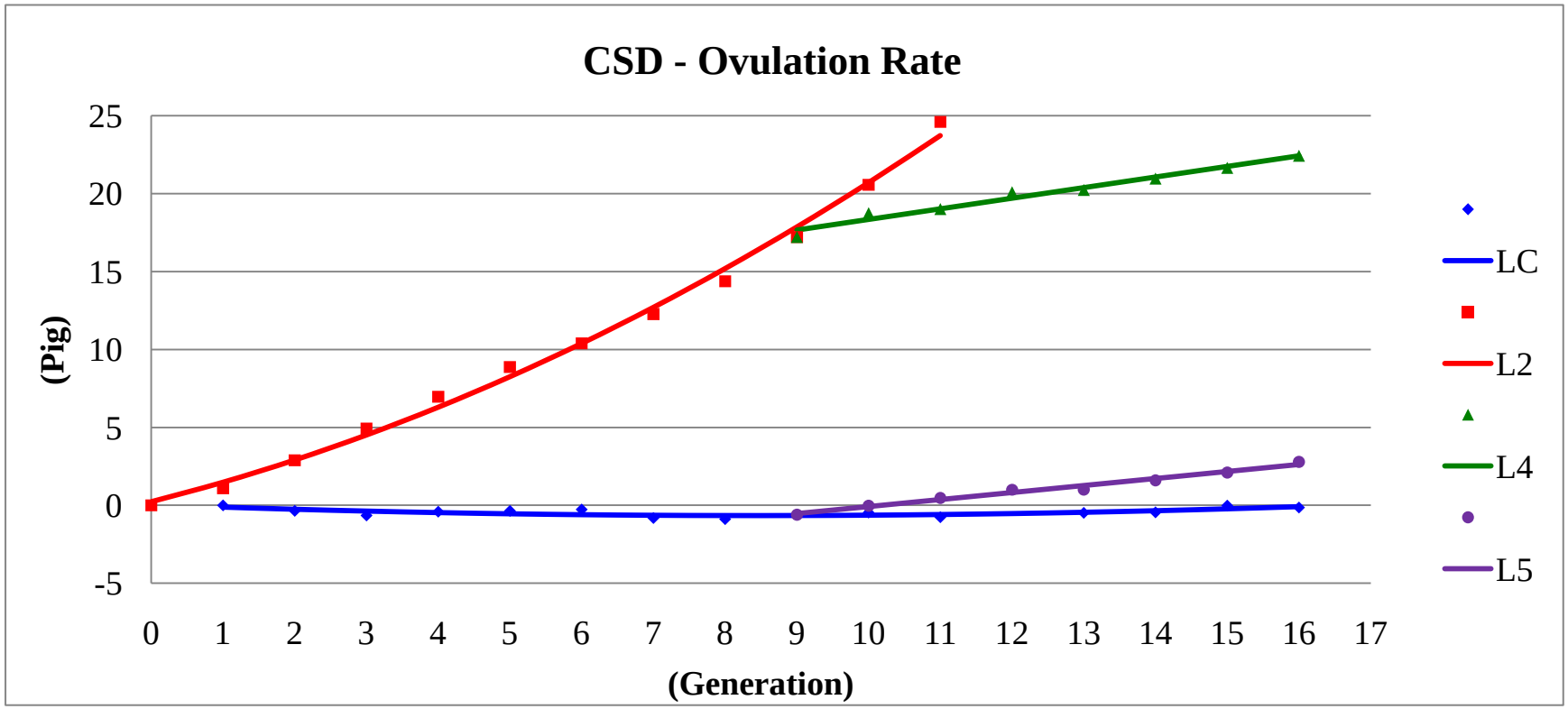

Figure 2.1. **Trends of cumulative selection differentials on generation for ovulation rate by line[a]**

[a] Lines:

LC was a control line in generation 0-16;

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11;

L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16.

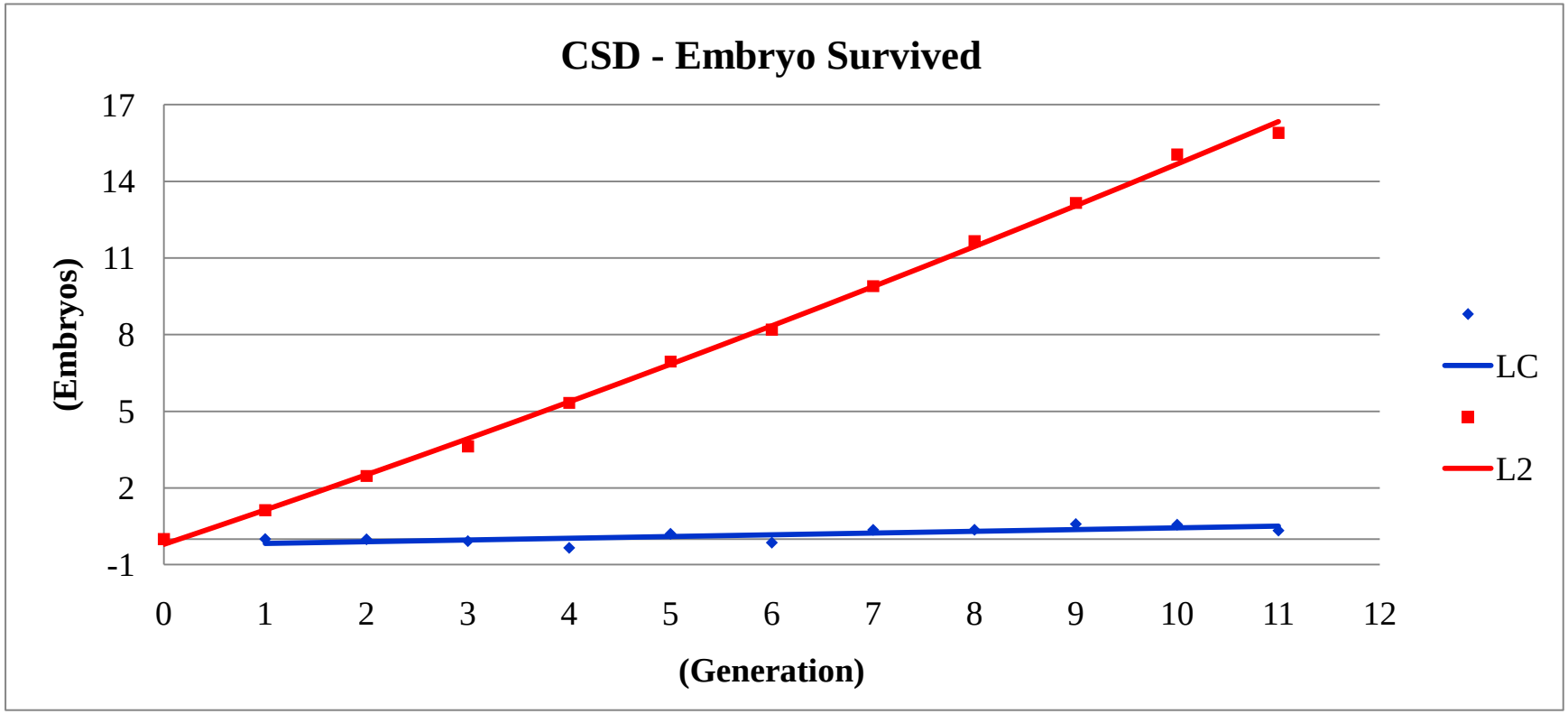

Figure 2.2. **Trends of cumulative selection differentials on generation for number of embryos survived by line[a]**

[a] Lines:

LC was a control line in generation 0-11;

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11.

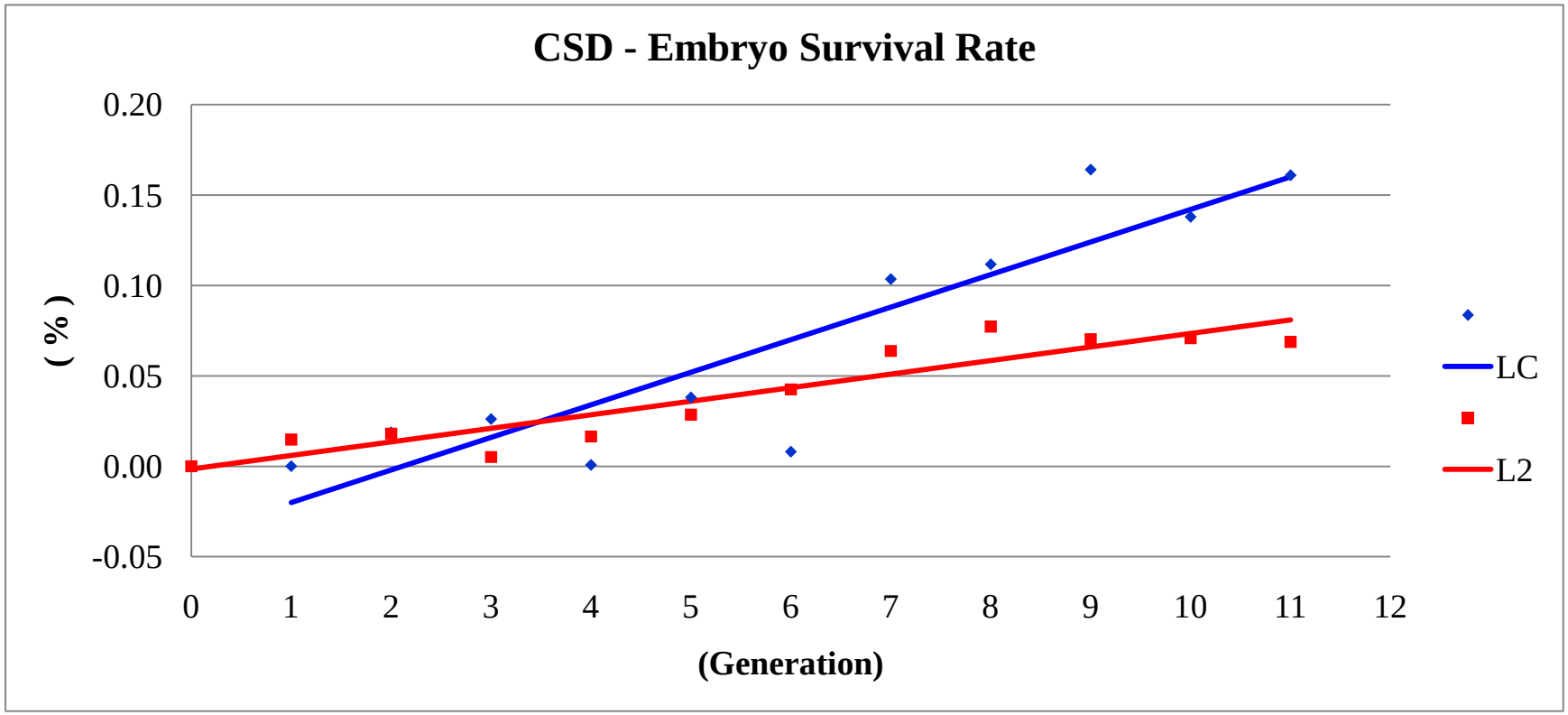

Figure 2.3. **Trends of cumulative selection differentials on generation for embryo survival rate by line[a]**

[a] Lines:

LC was a control line in generation 0-11;

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11.

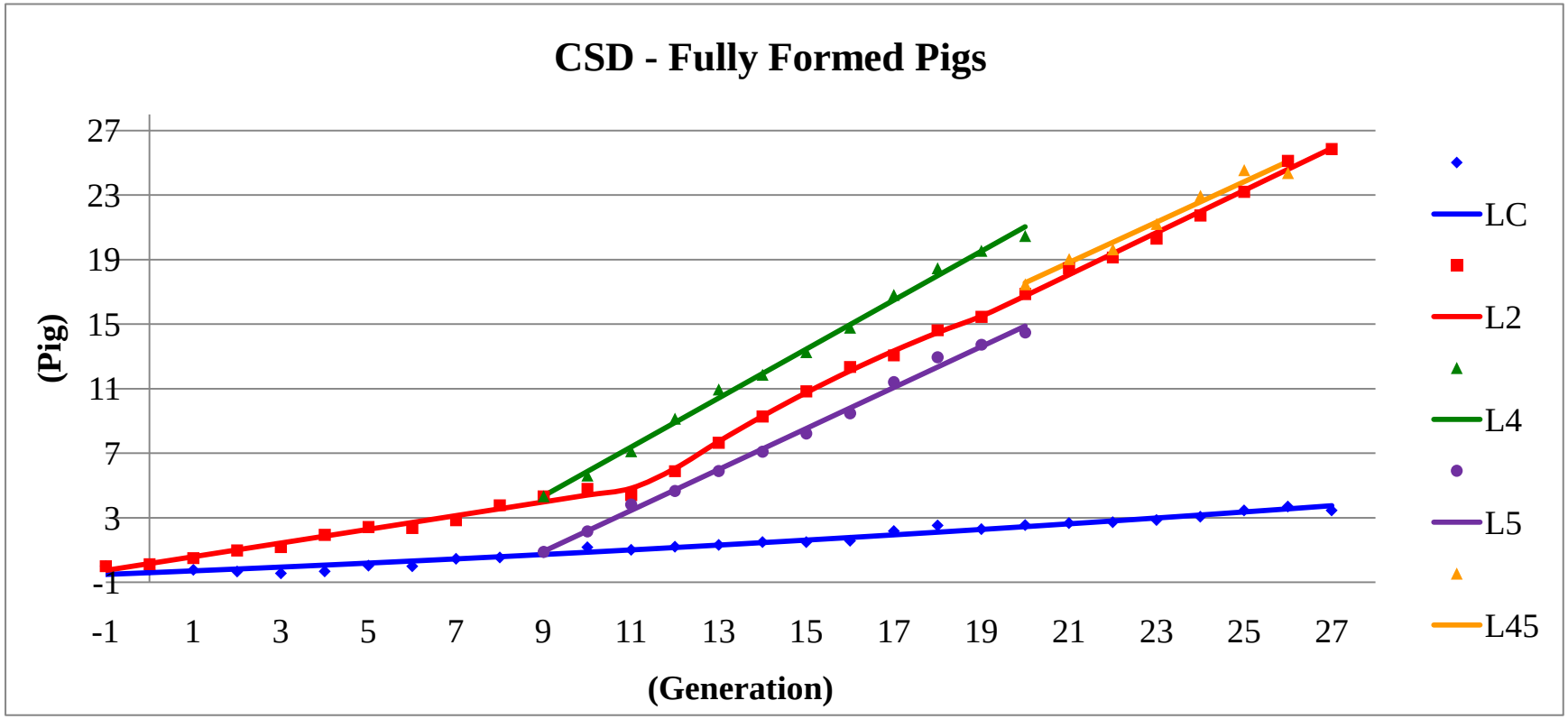

Figure 2.4. **Trends of cumulative selection differentials on generation for number of fully formed pigs per litter by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

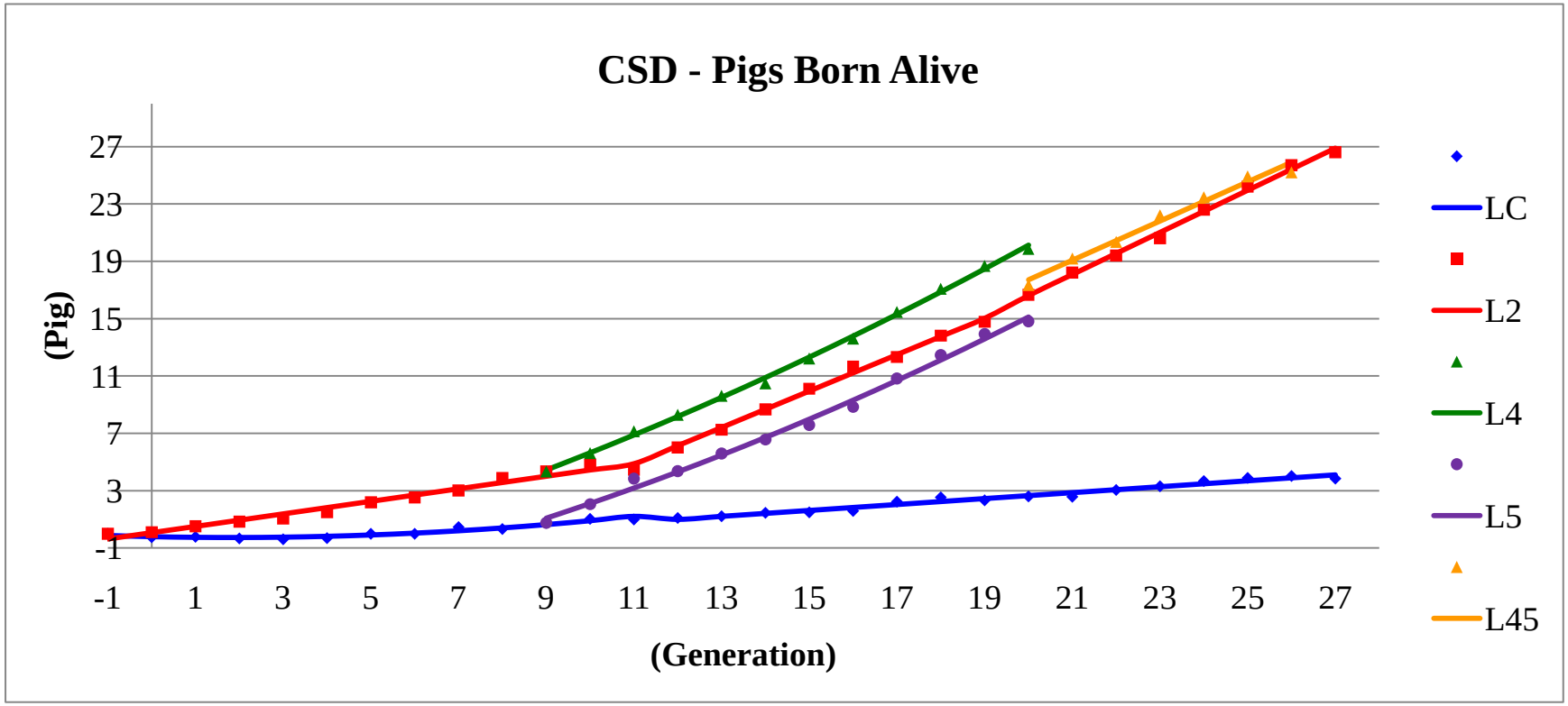

Figure 2.5. **Trends of cumulative selection differentials on generation for number of pigs born alive per litter by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

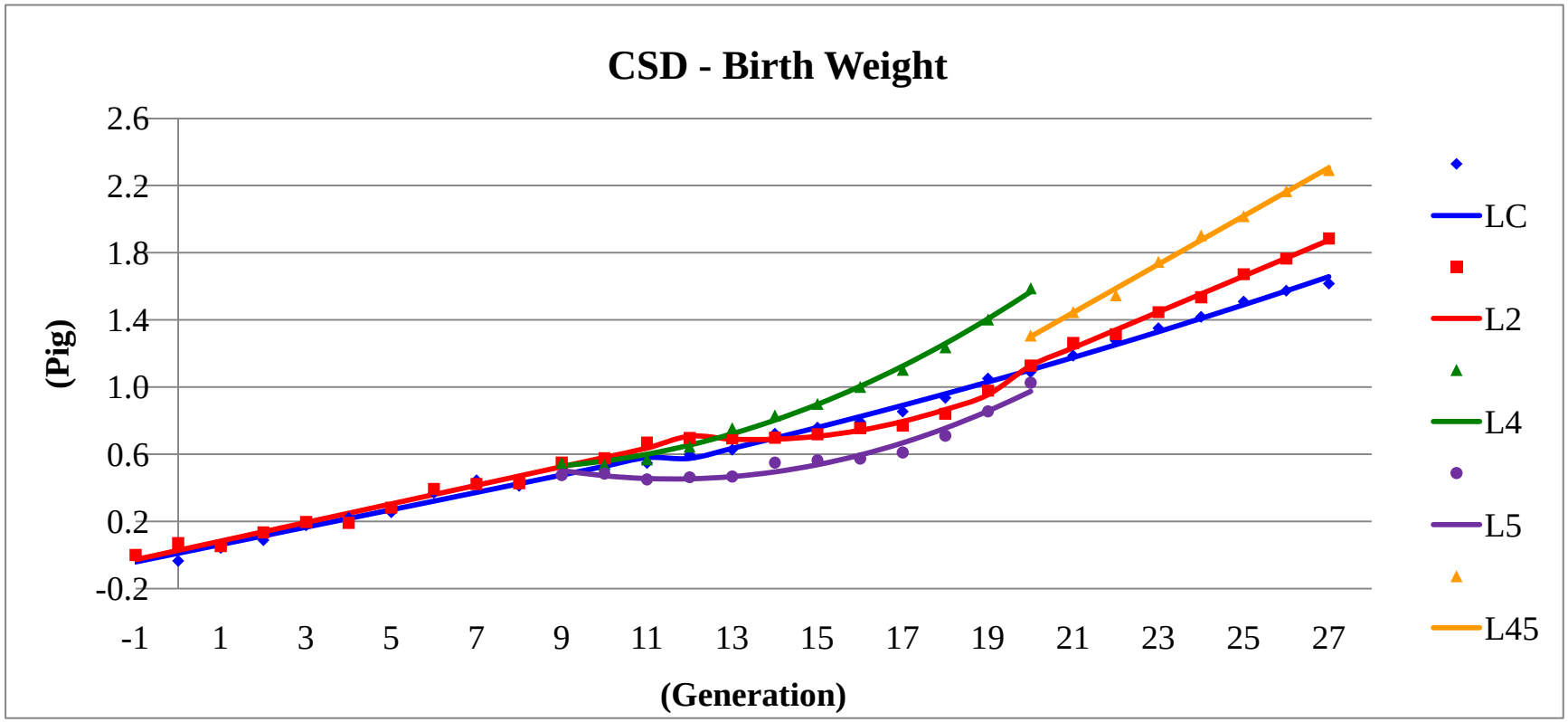

Figure 2.6. **Trends of cumulative selection differentials on generation for birth weight by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

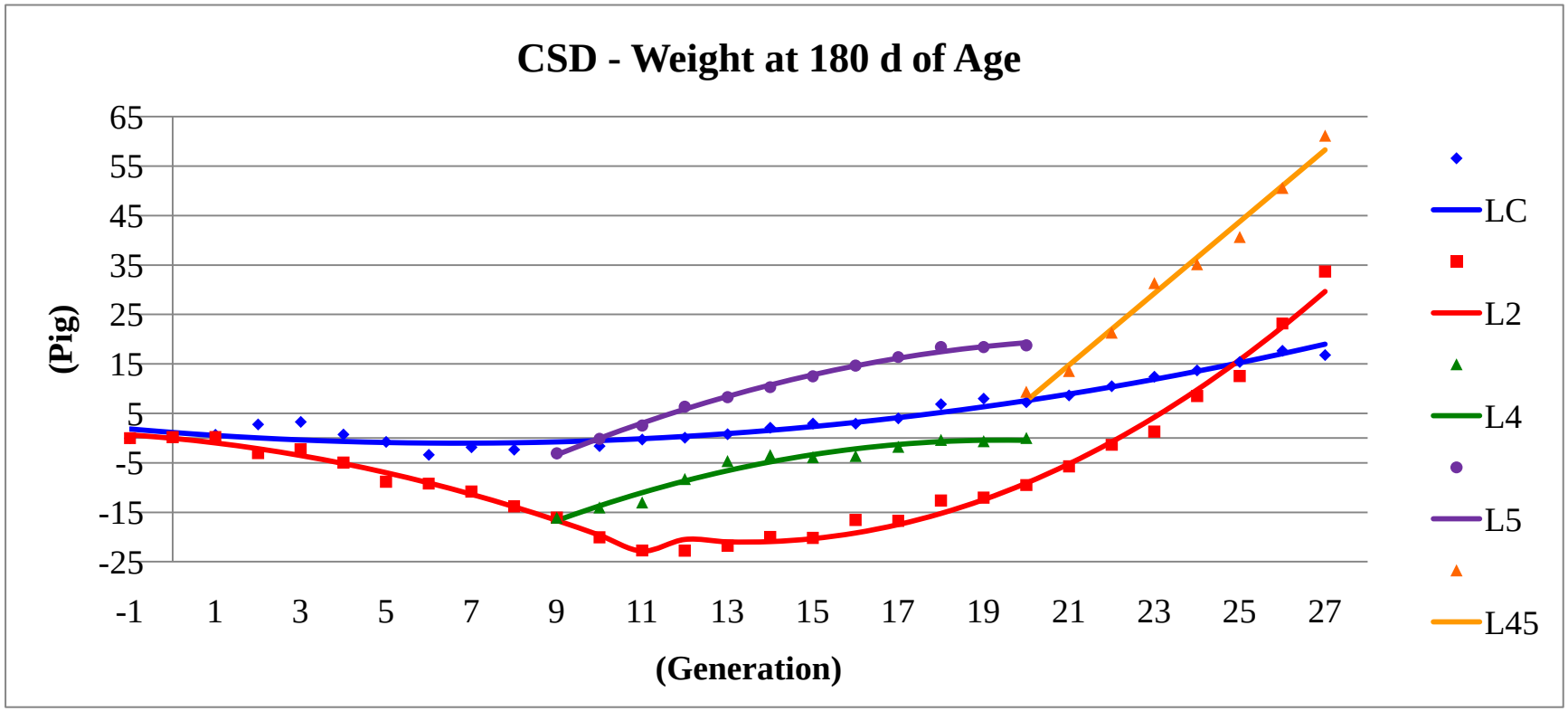

Figure 2.7. **Trends of cumulative selection differentials on generation for weight at 180 days of age by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

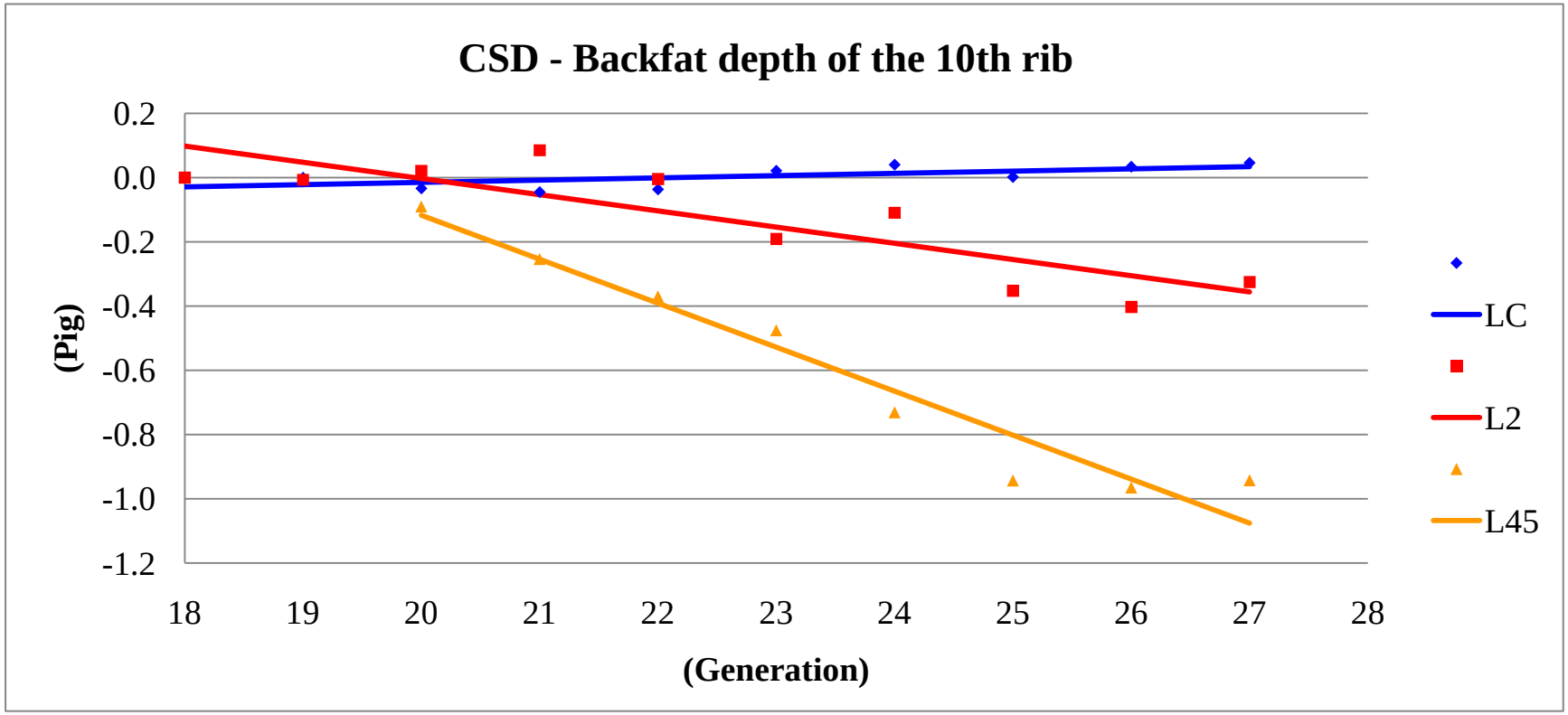

Figure 2.8. **Trends of cumulative selection differentials on generation for backfat depth of the 10th rib at age of final weight by line[a]**

[a] Lines:

LC was a control line in generation 18-28;

L2 was for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

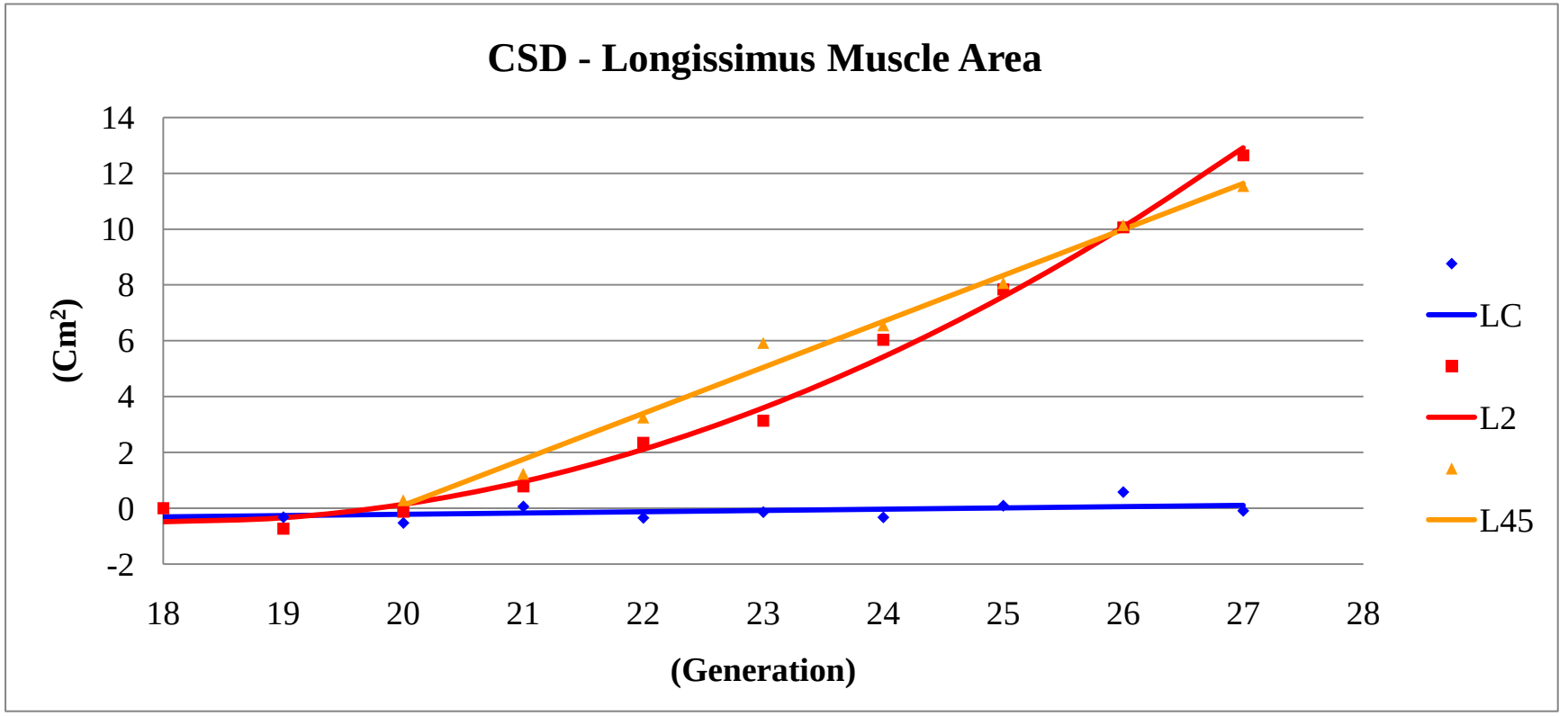

Figure 2.9. **Trends of cumulative selection differentials on generation for longissimus muscle area at age of final weight by line[a]**

[a] Lines:

LC was a control line in generation 18-28;

L2 was for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

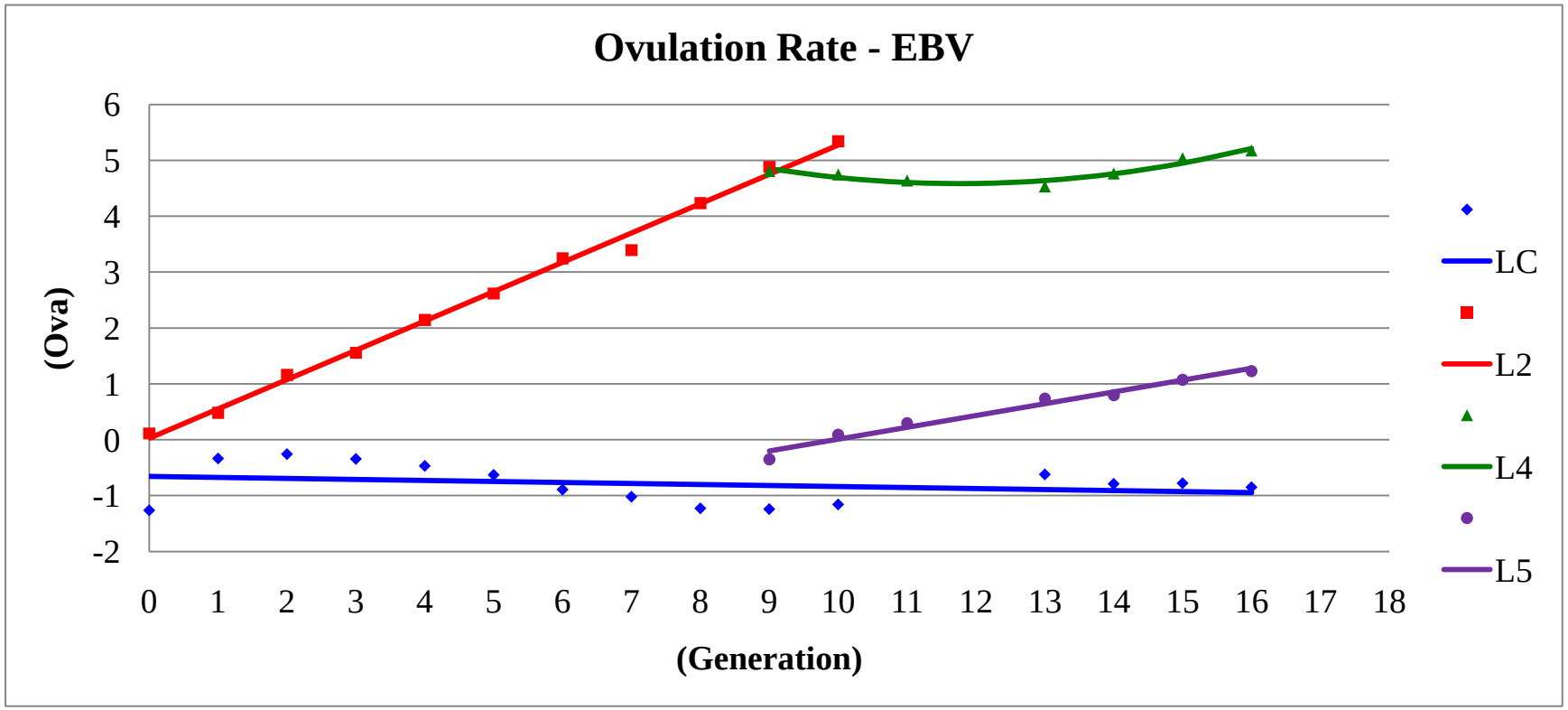

Figure 3. **Estimated genetic trends for ovulation rate by line[a]**

[a] Lines:

LC was a control line in generation 0-16;

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11;

L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16.

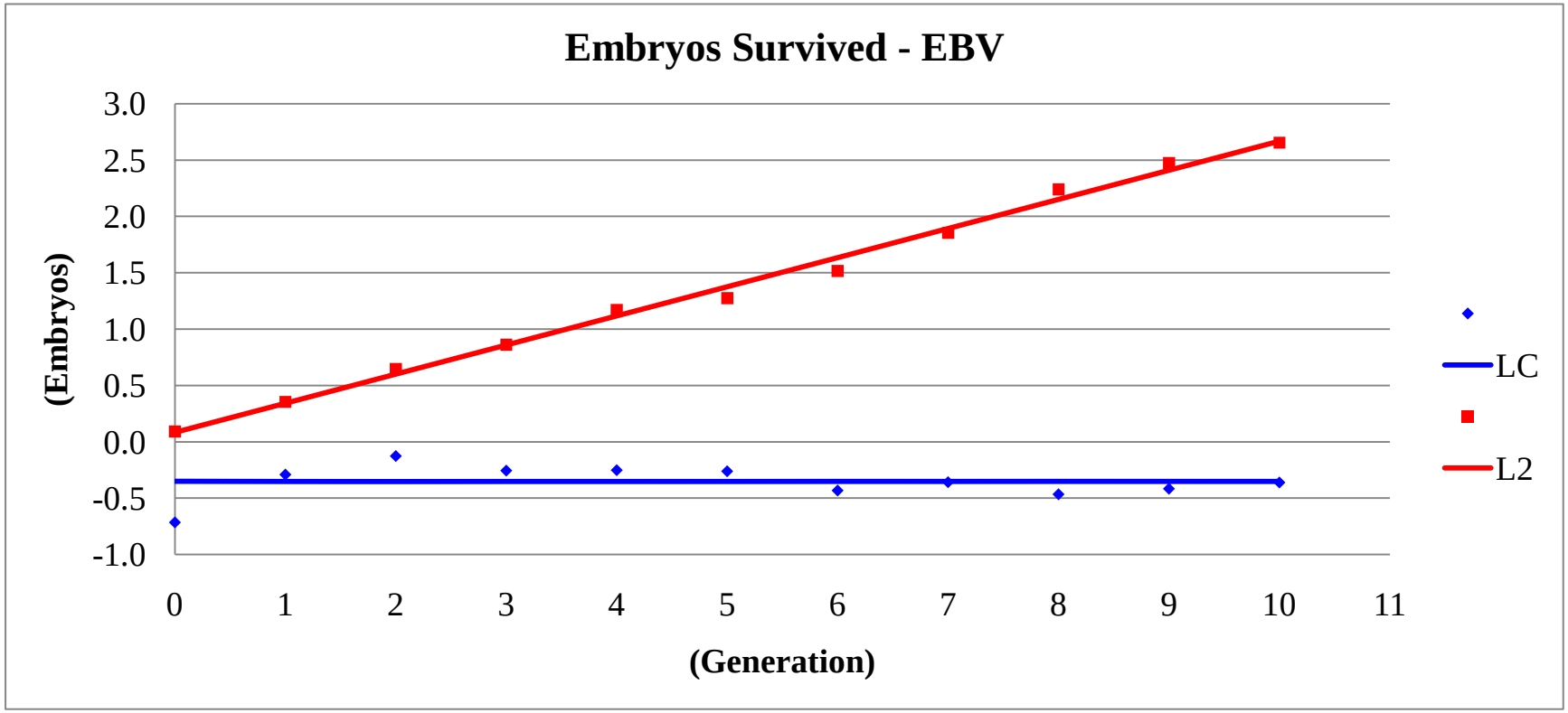

***Figure 4*. Estimated genetic trends for number of embryos survived by line[a]**

[a] Lines:

LC was a control line in generation 0-11;

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11.

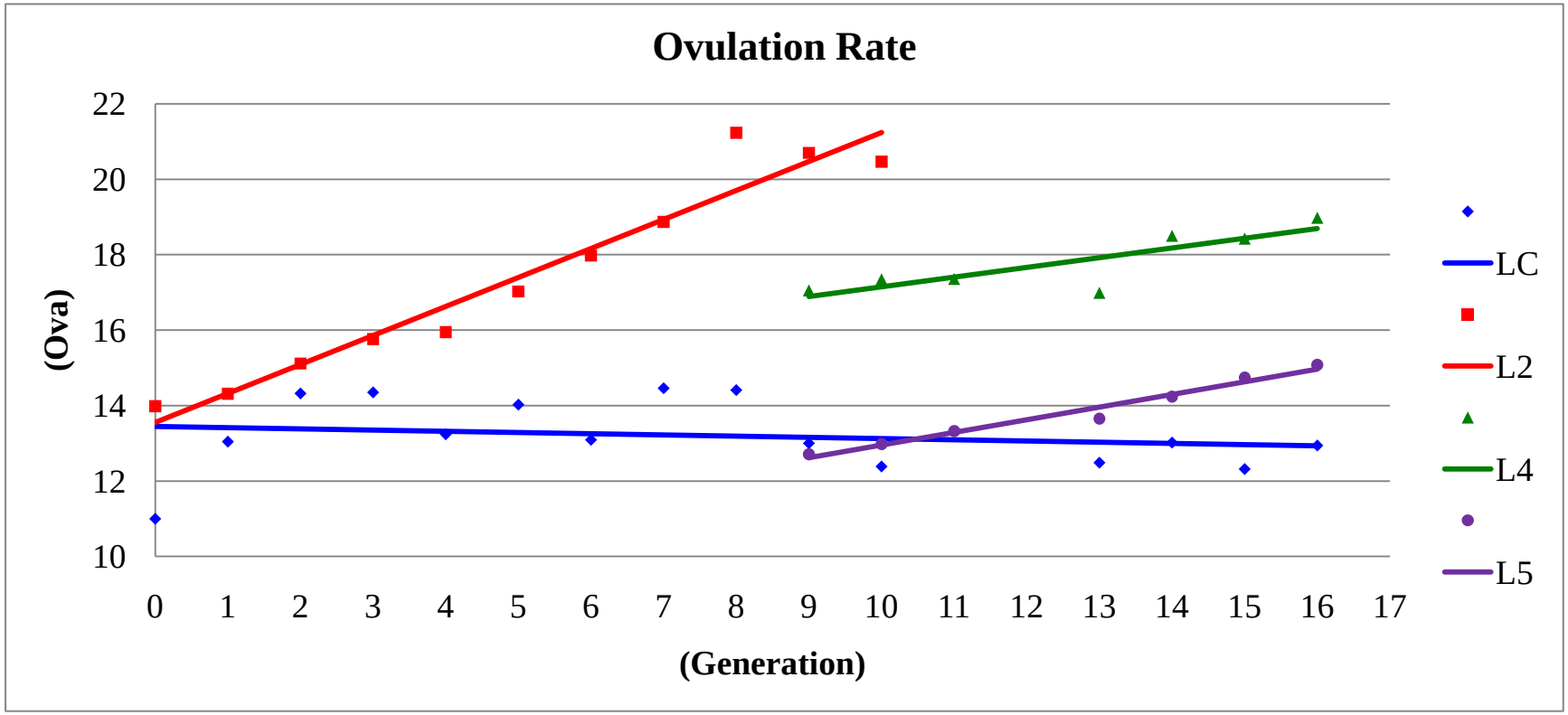

Figure 5. **Estimated phenotypic trends for ovulation rate by line[a]**

[a] Lines:

LC was a control line in generation 0-16;

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11;

L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16.

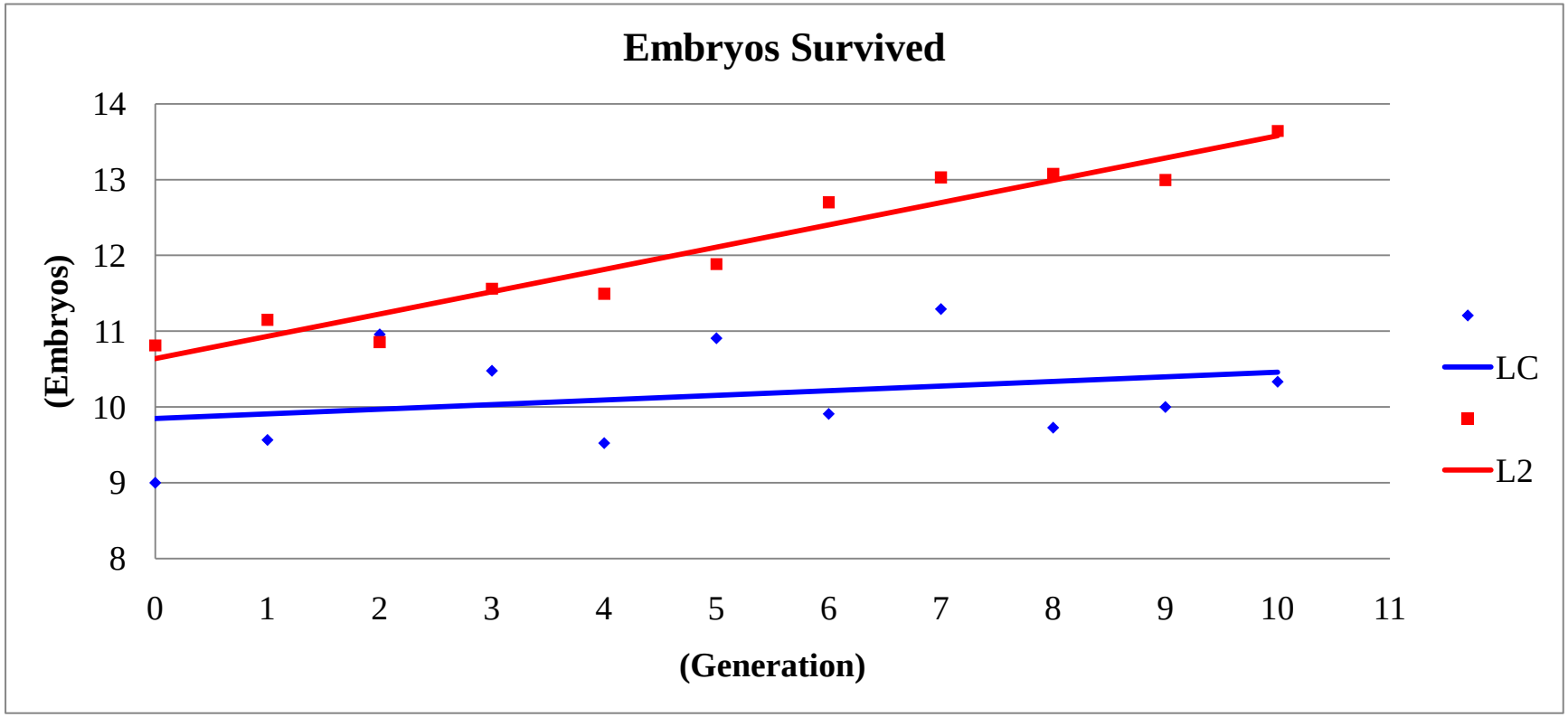

Figure 6. **Estimated phenotypic trends for number of embryos survived by line[a]**

[a] Lines:

LC was a control line in generation 0-11;

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11.

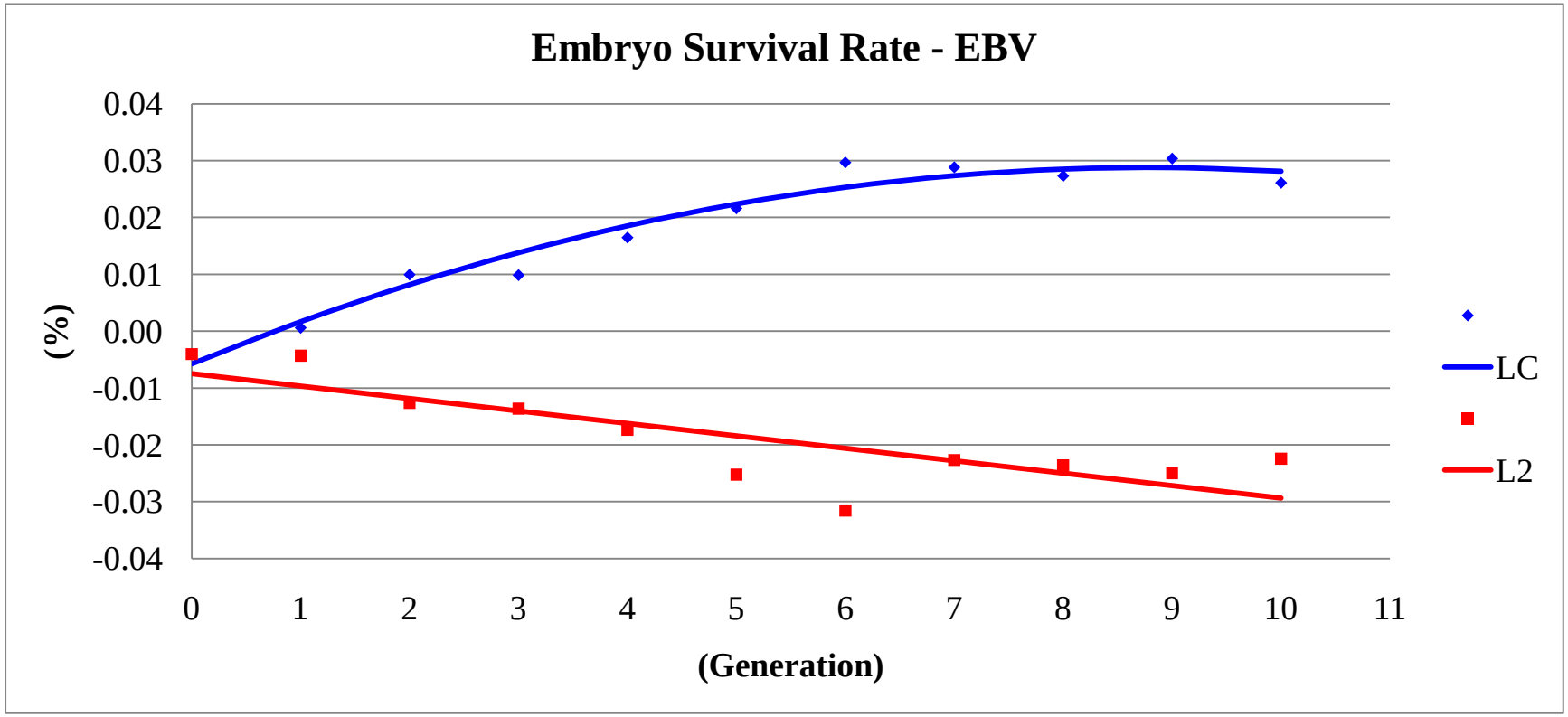

Figure 7. **Estimated genetic trends for embryo survival rate by line[a]**

[a] Lines:

LC was a control line in generation 0-11;

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11.

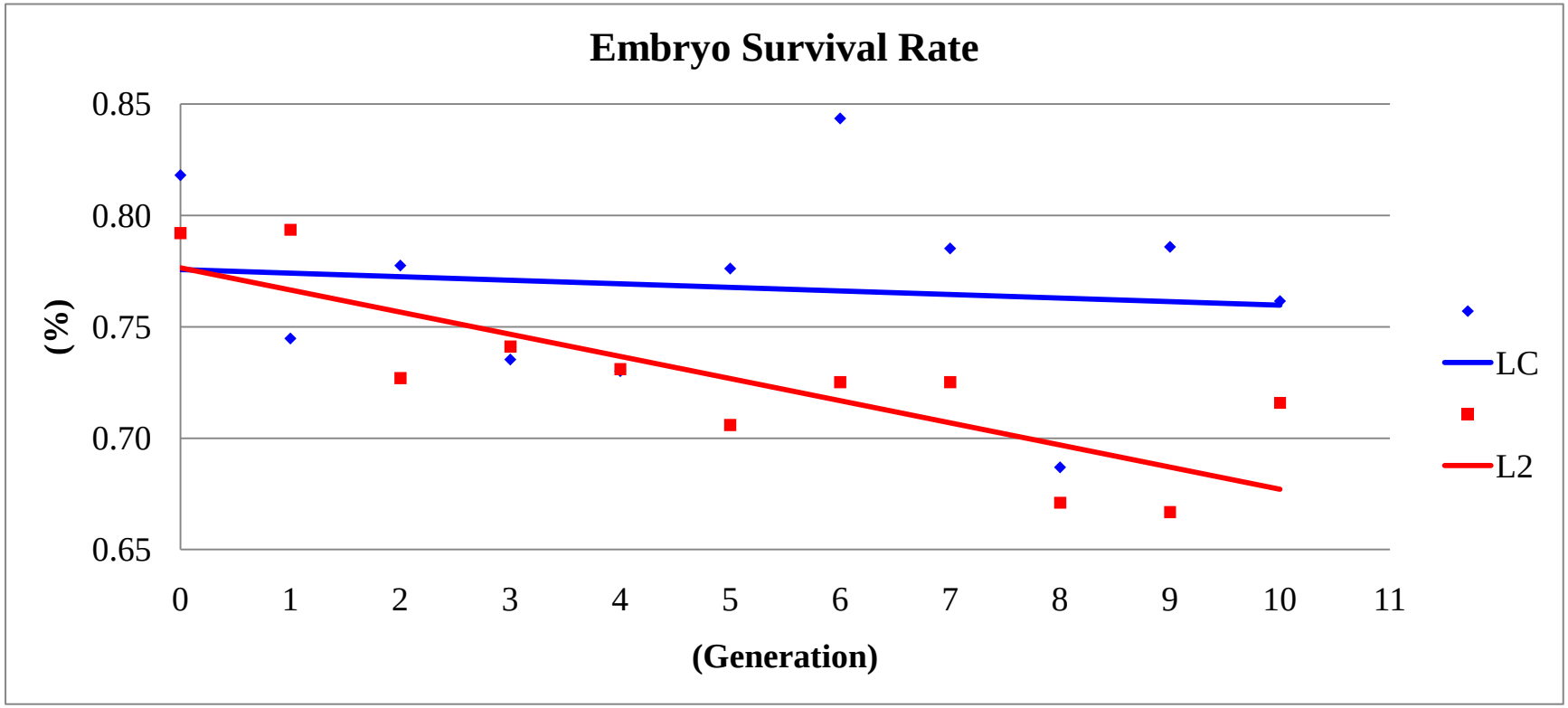

Figure 8. **Estimated phenotypic trends for embryo survival rate by line[a]**

[a] Lines:

LC was a control line in generation 0-11;

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11.

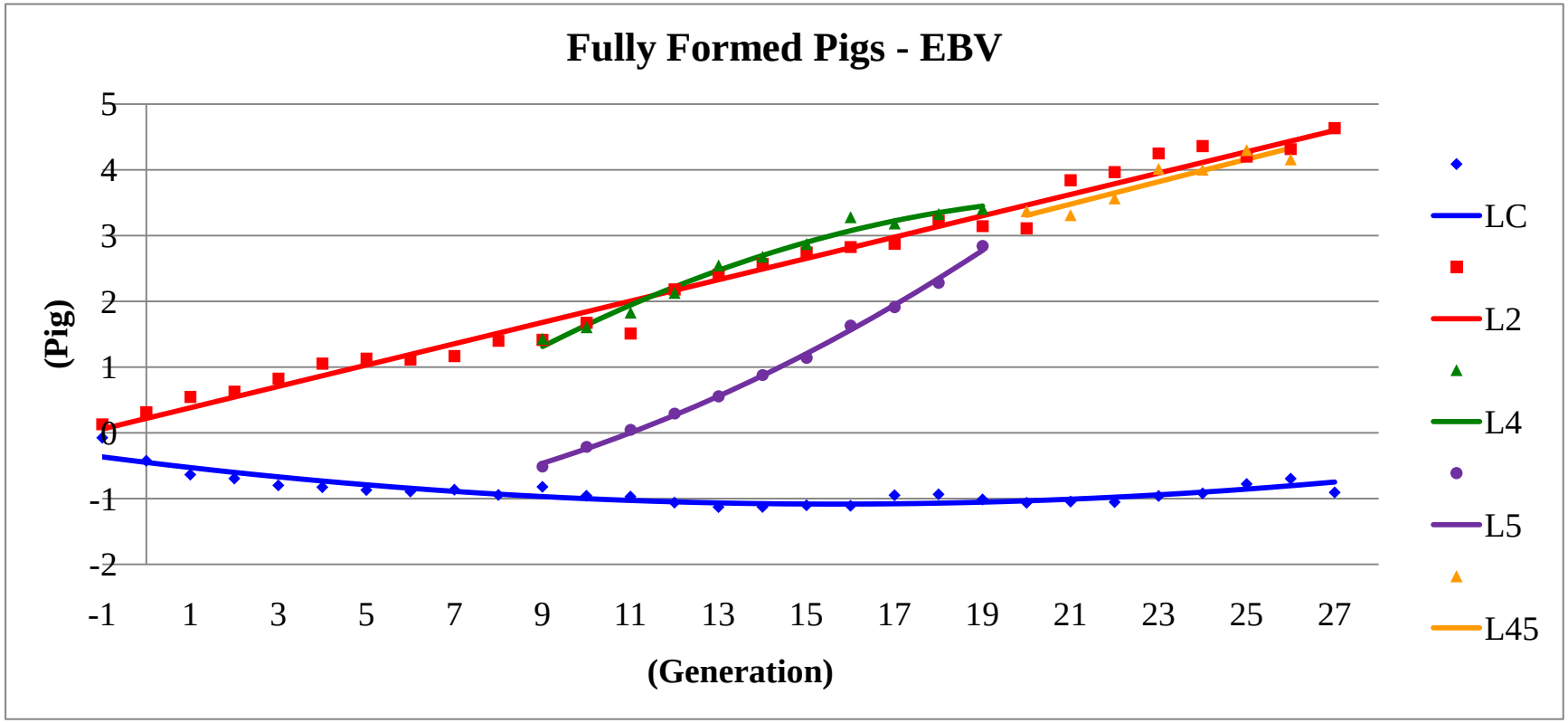

Figure 9. **Estimated genetic trends for number of fully formed pigs per litter by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

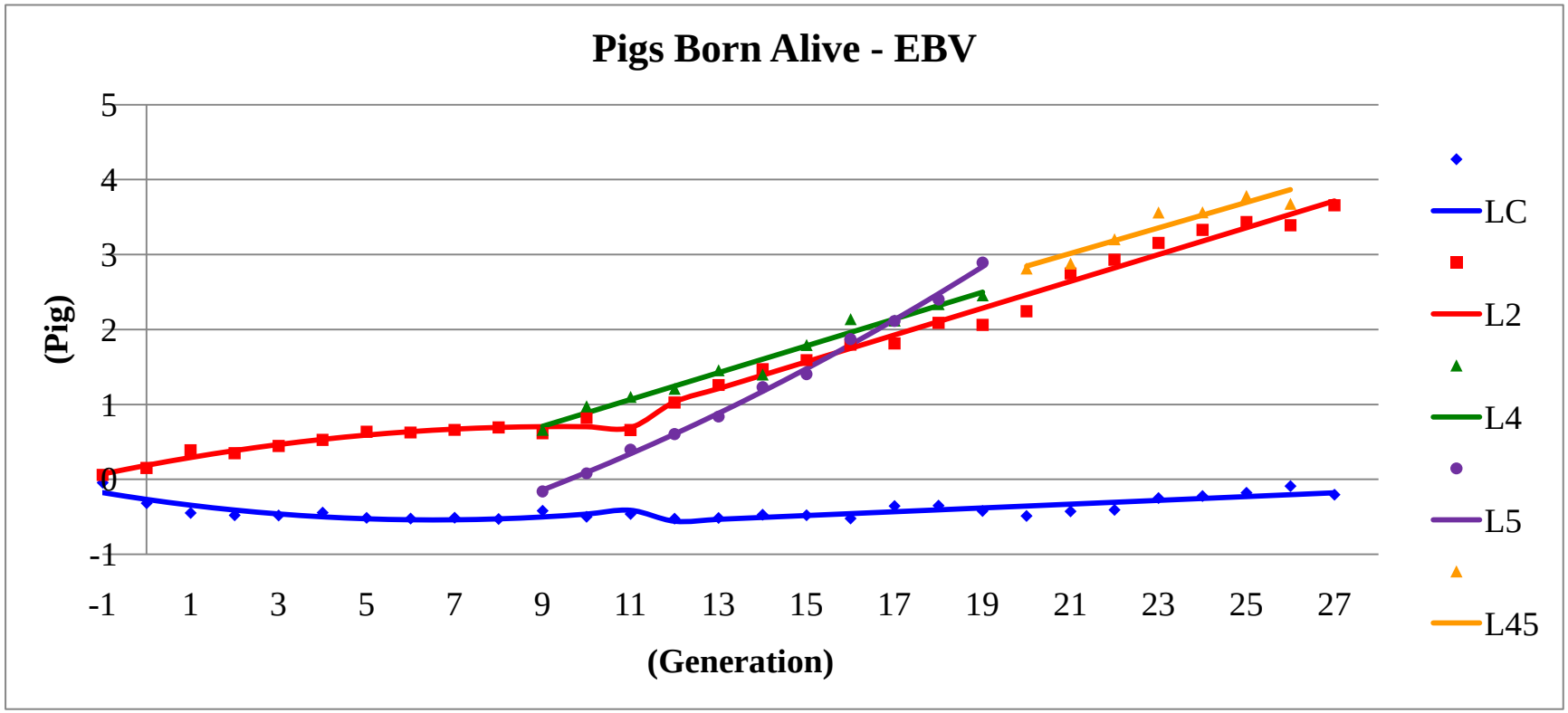

Figure 10. **Estimated genetic trends for number of pigs born alive per litter by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

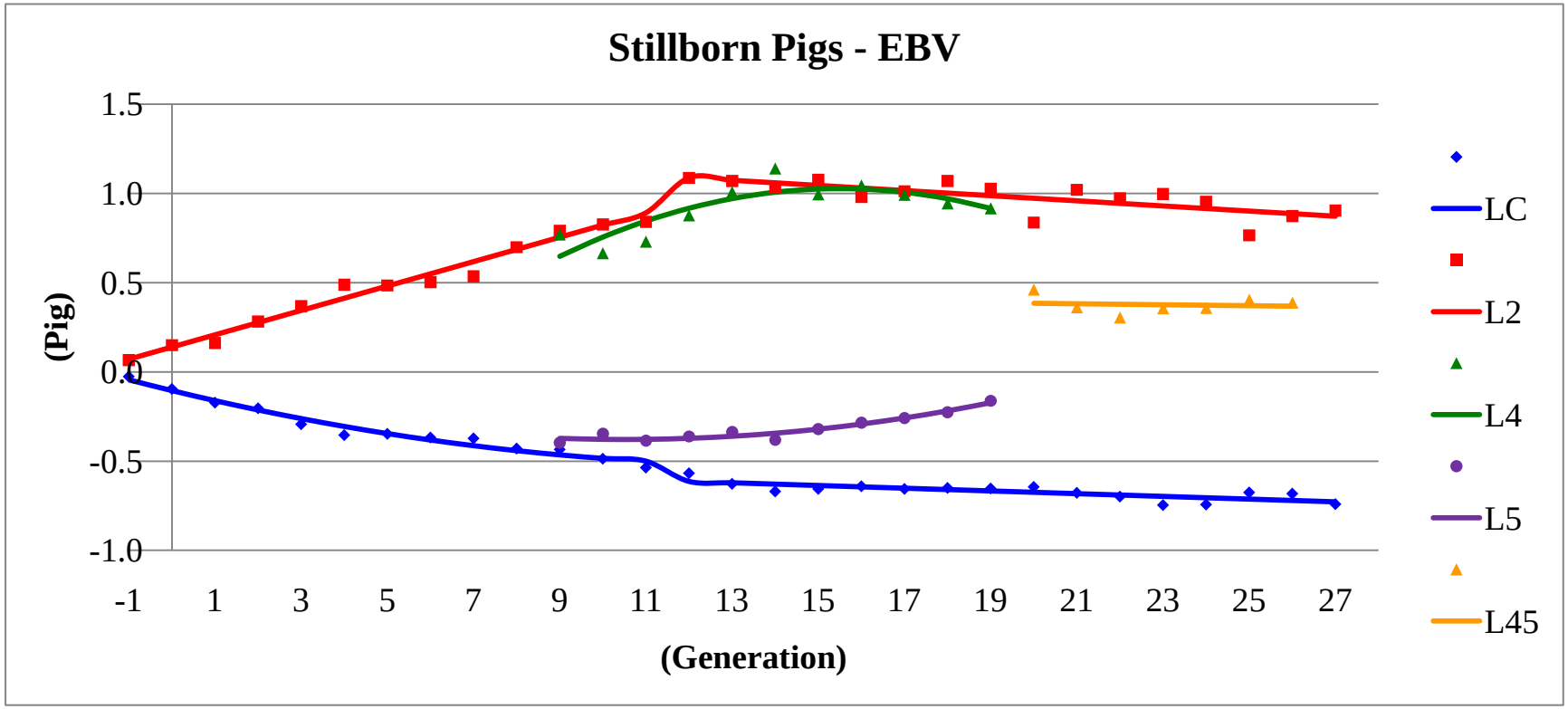

Figure 11. **Estimated genetic trends for number of stillborn pigs per litter by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

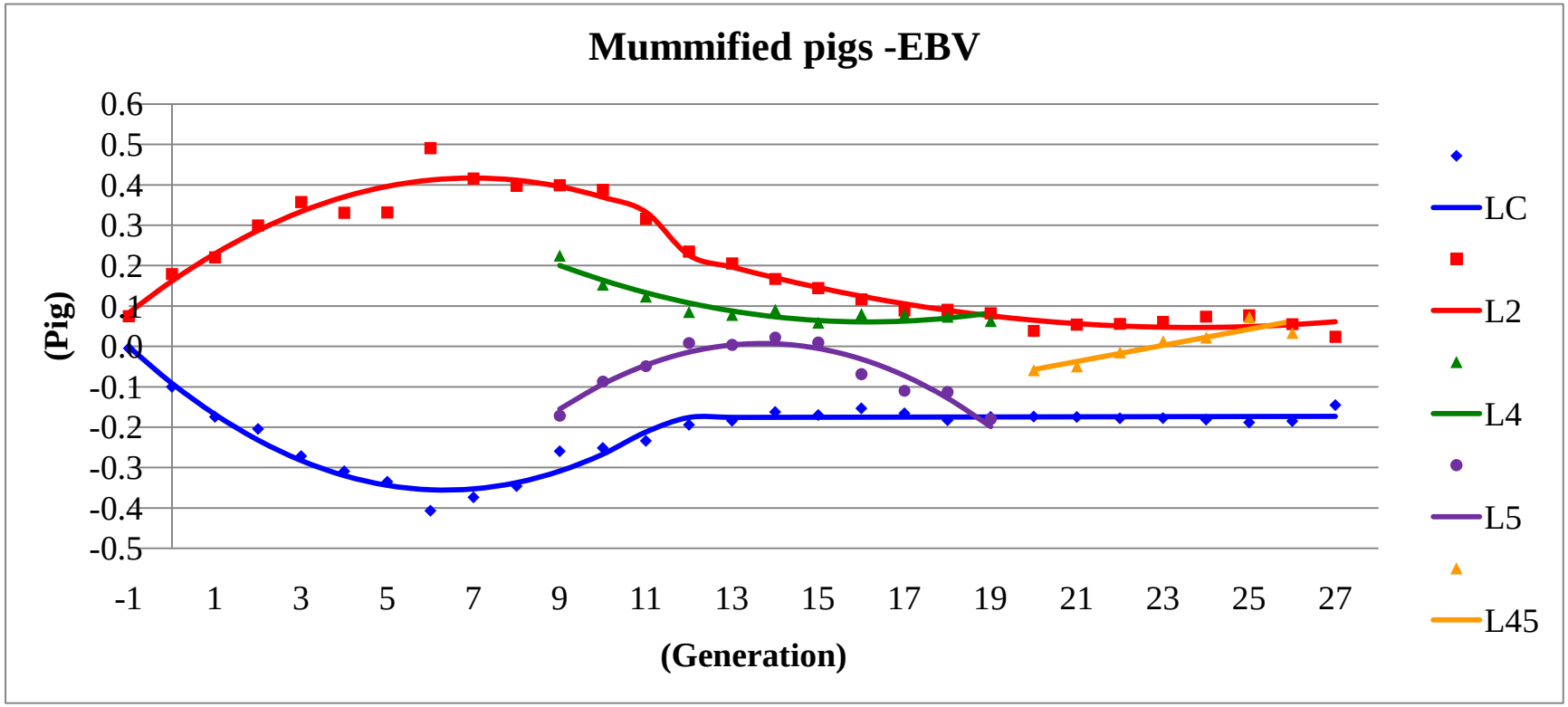

Figure 12. **Estimated genetic trends for number of mummified pigs per litter by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

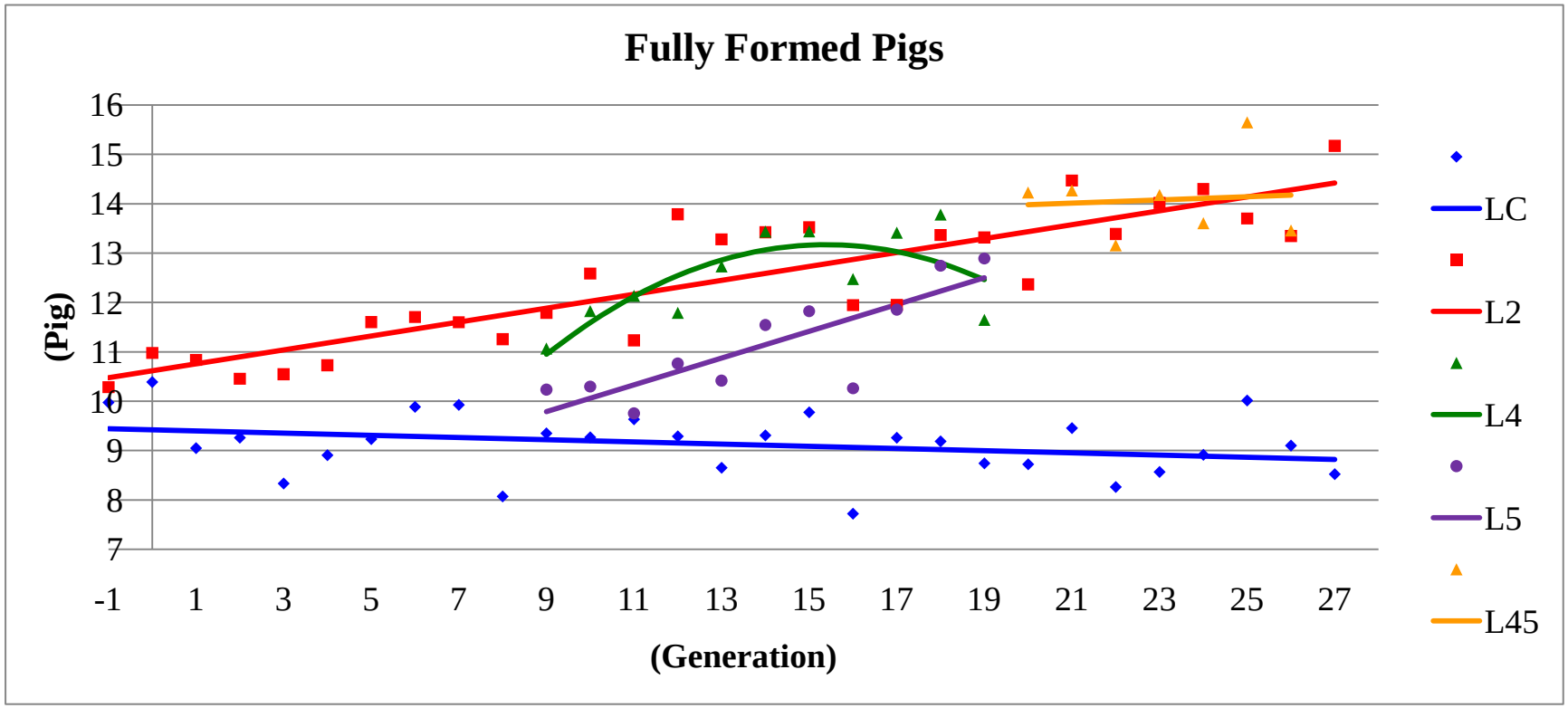

Figure 13. **Estimated phenotypic trends for number of fully formed pigs per litter by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

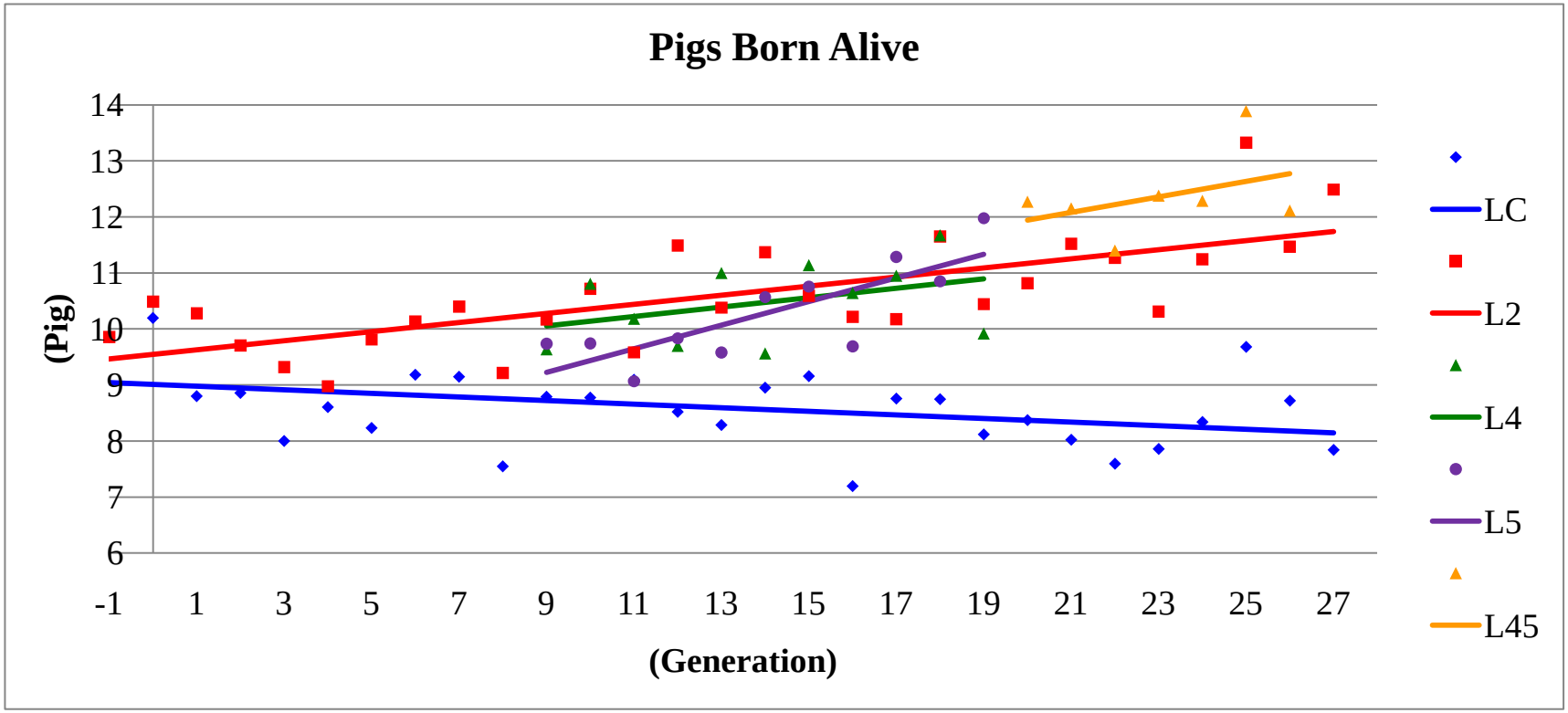

Figure 14. **Estimated phenotypic trends for number of born alive pigs per litter by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

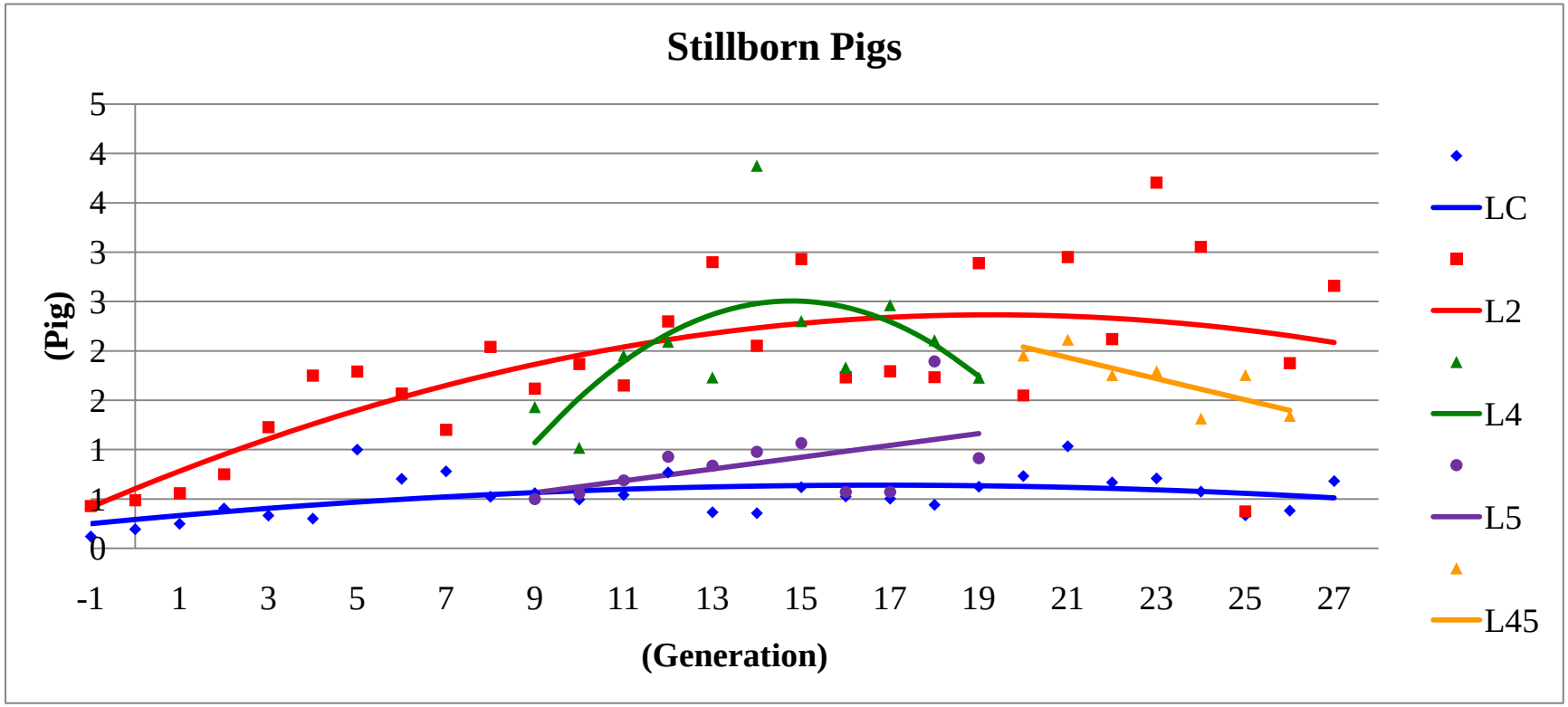

Figure 15. **Estimated phenotypic trends for number of stillborn pigs per litter by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

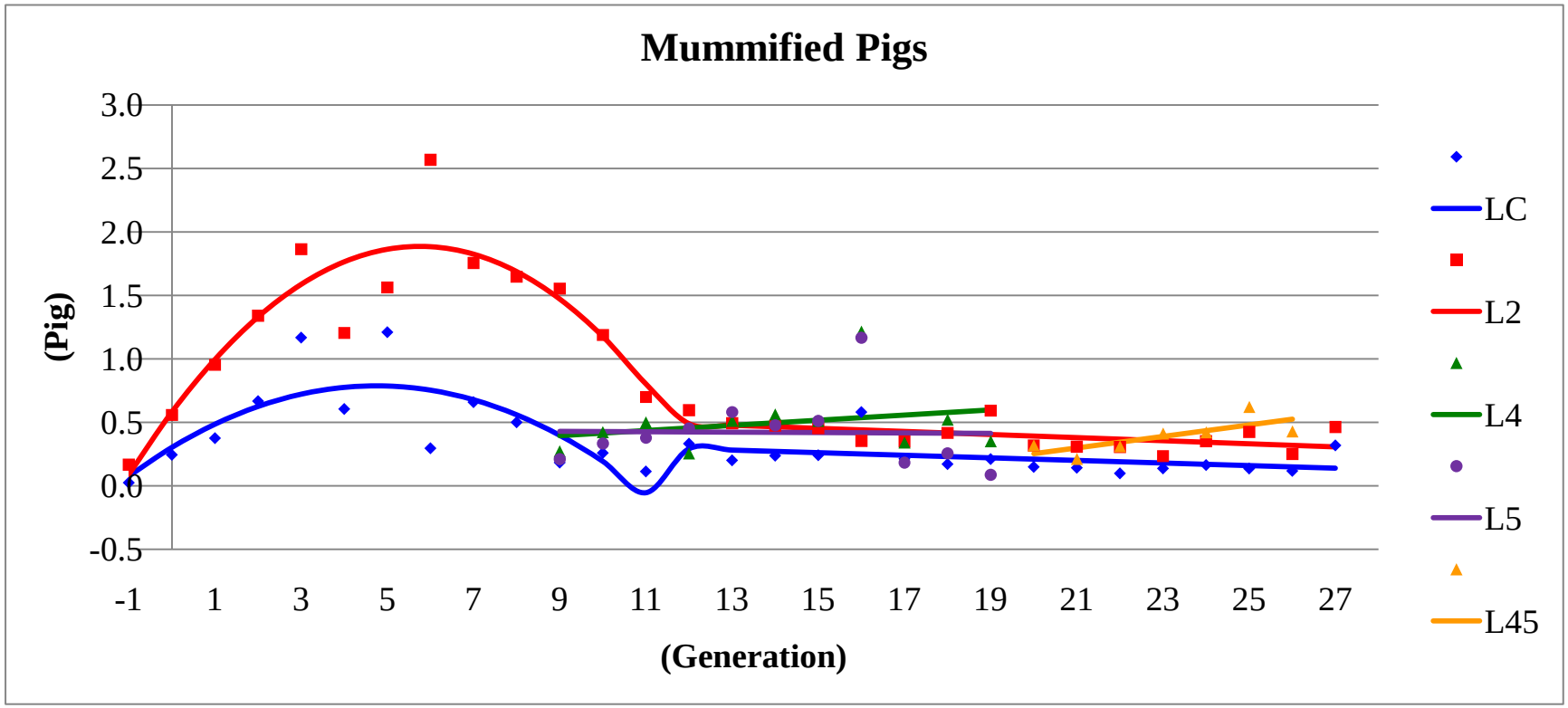

Figure 16. **Estimated phenotypic trends for number of mummified pigs per litter by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

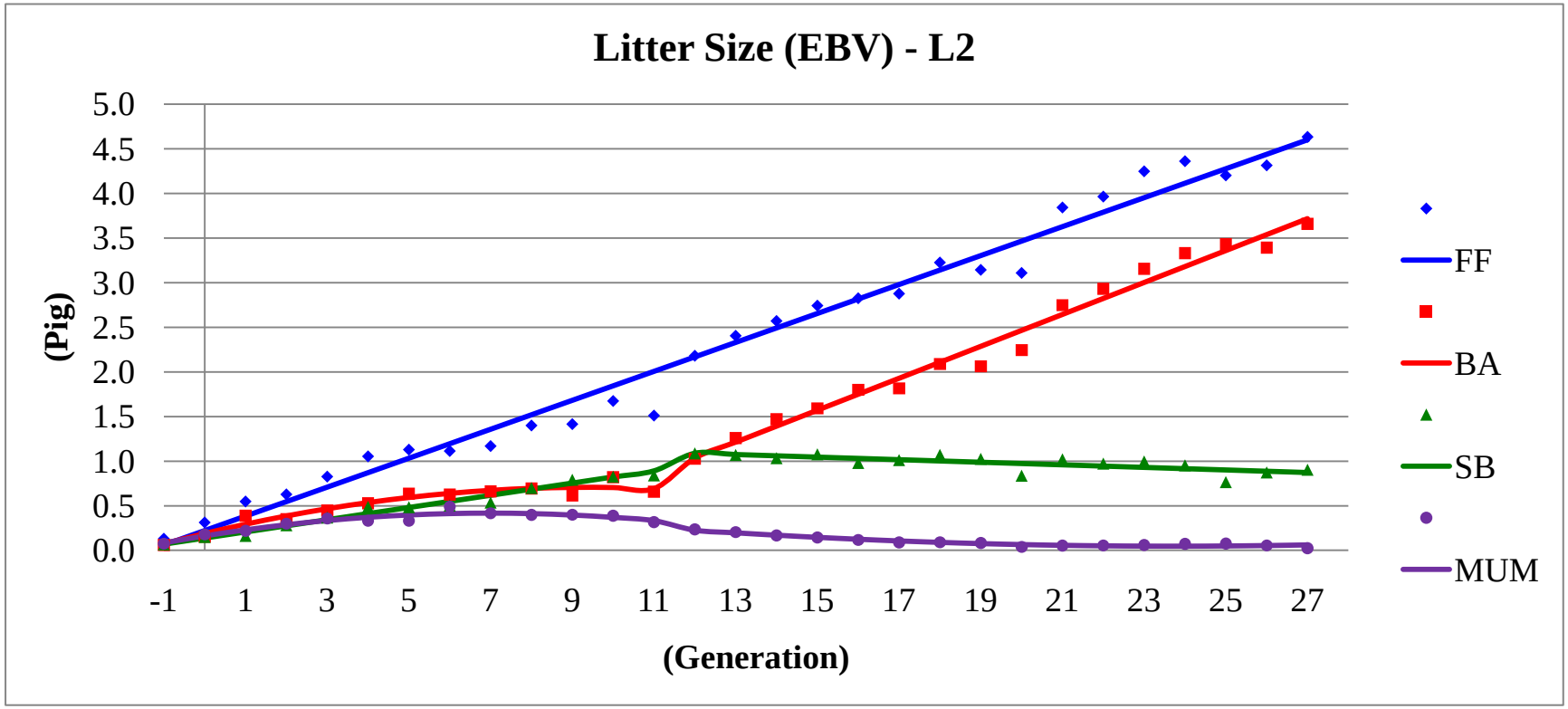

Figure 17.1. **Estimated genetic trends for number of fully form pigs, pigs born alive, stillborn pigs and mummified pigs per litter in selection line 2[a]**

[a] Line:

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28.

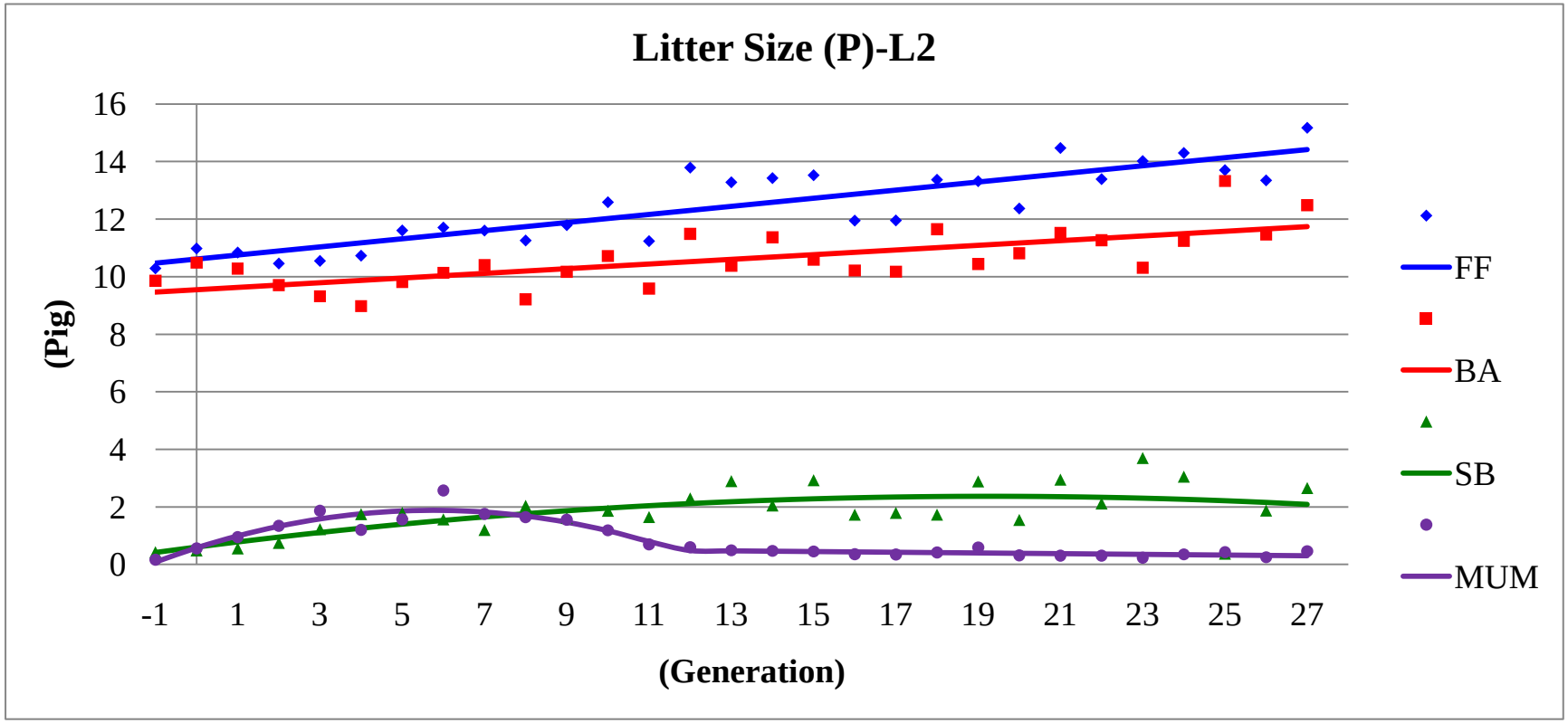

Figure 17.2. **Estimated genetic trends for number of fully form pigs, pigs born alive, stillborn pigs and mummified pigs per litter in selection line 2[a]**

[a] Line:

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28.

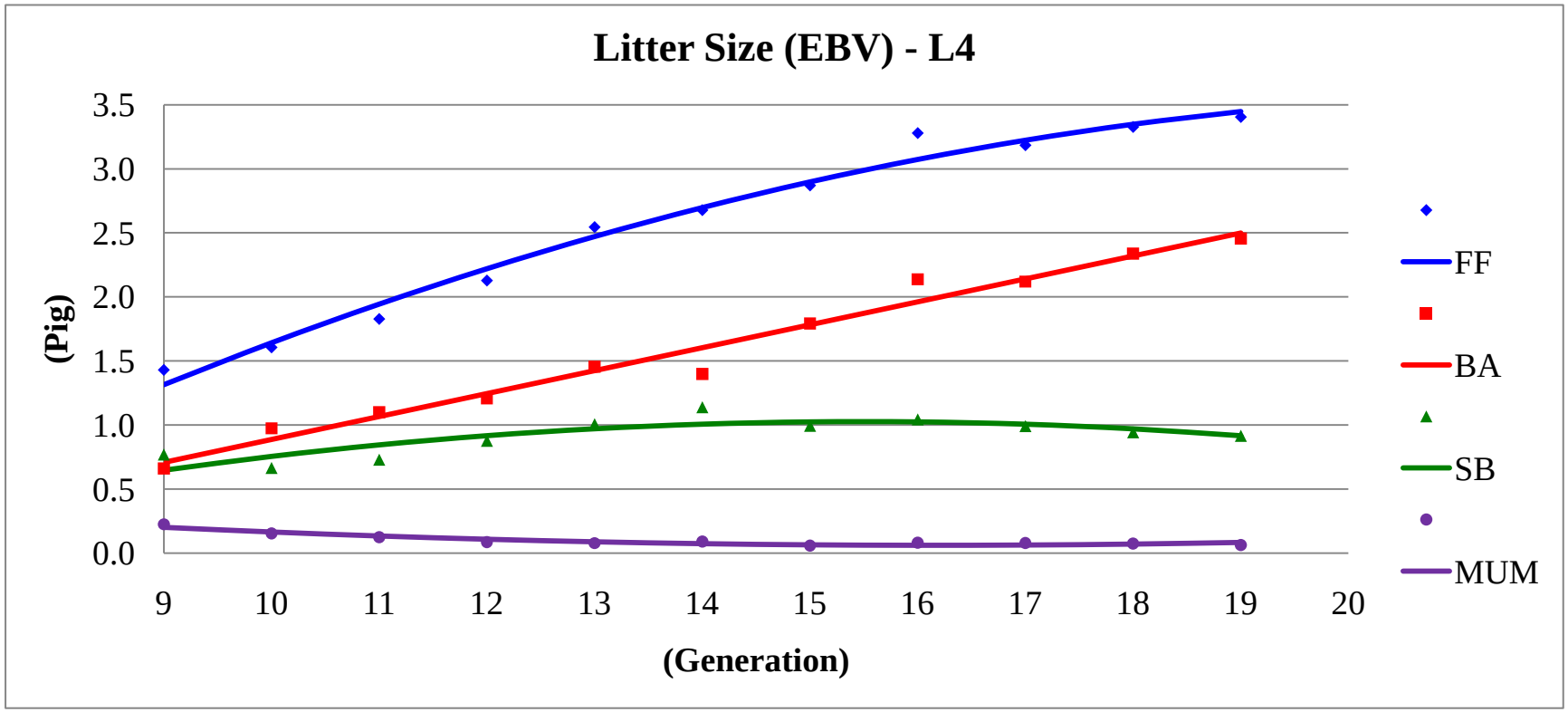

Figure 17.3. **Estimated genetic trends for number of fully form pigs, pigs born alive, stillborn pigs and mummified pigs per litter in selection line 4[a]**

[a] Line:

L4 was selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19.

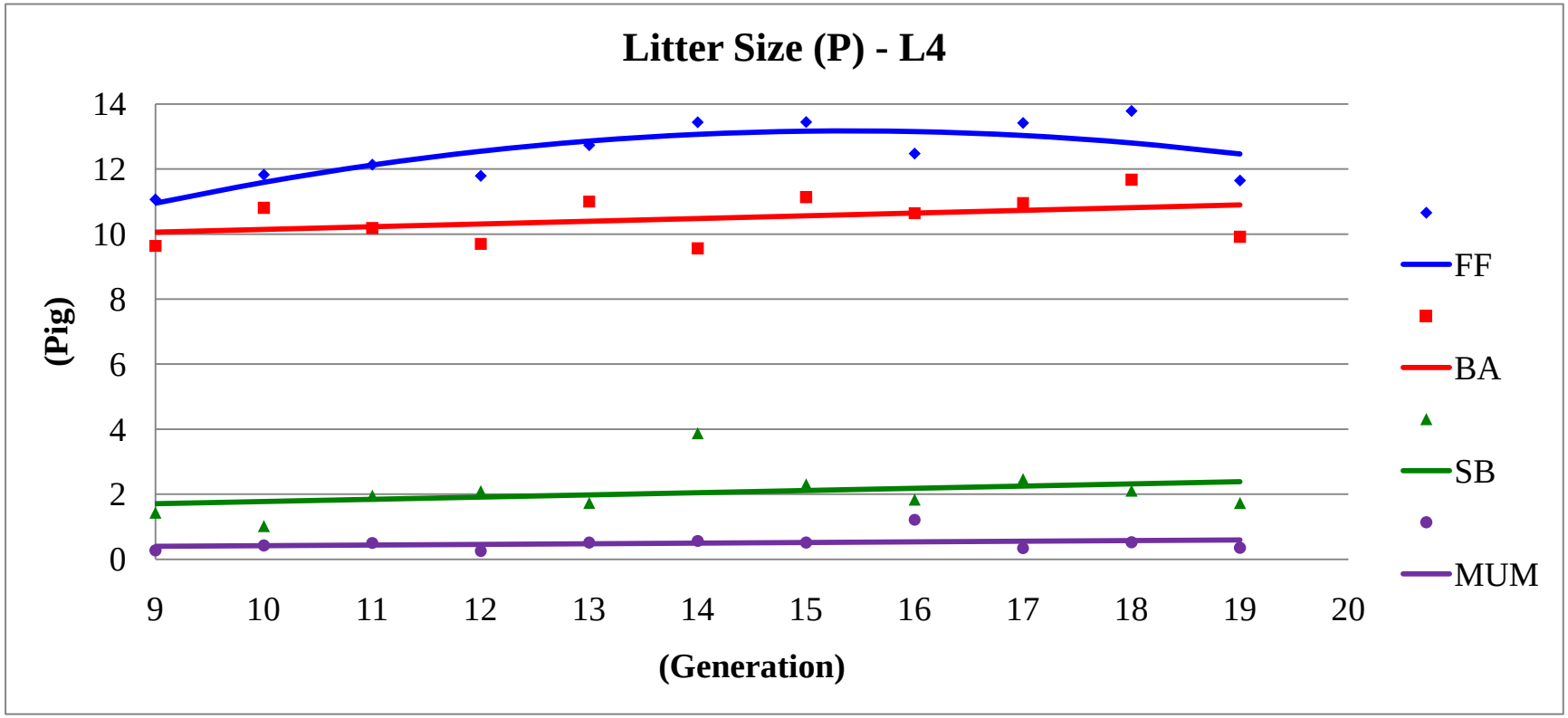

Figure 17.4. **Estimated genetic trends for number of fully form pigs, pigs born alive, stillborn pigs and mummified pigs per litter in selection line 4[a]**

[a] Line:

L4 was selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19.

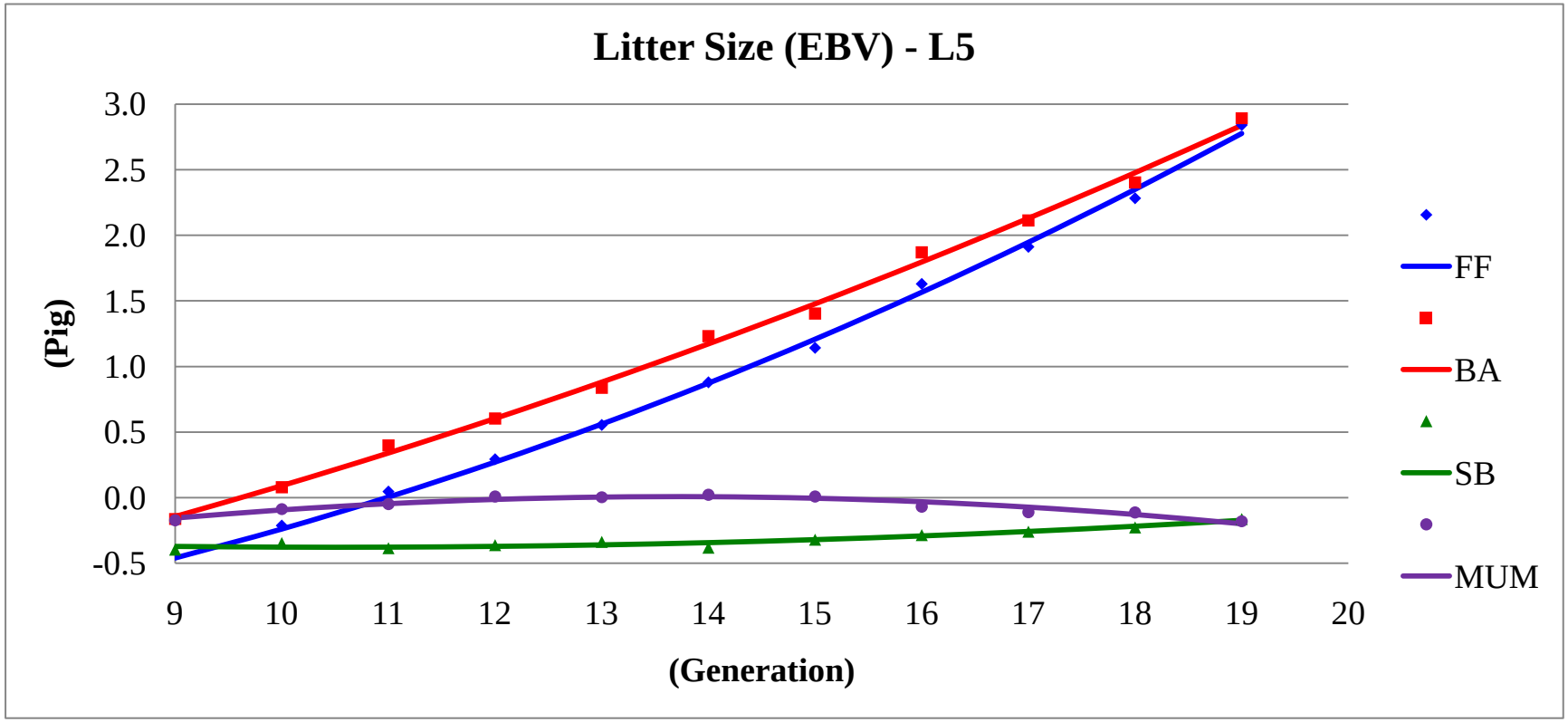

Figure 17.5. **Estimated genetic trends for number of fully form pigs, pigs born alive, stillborn pigs and mummified pigs per litter in selection line 5[a]**

[a] Line:

L5 was selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19.

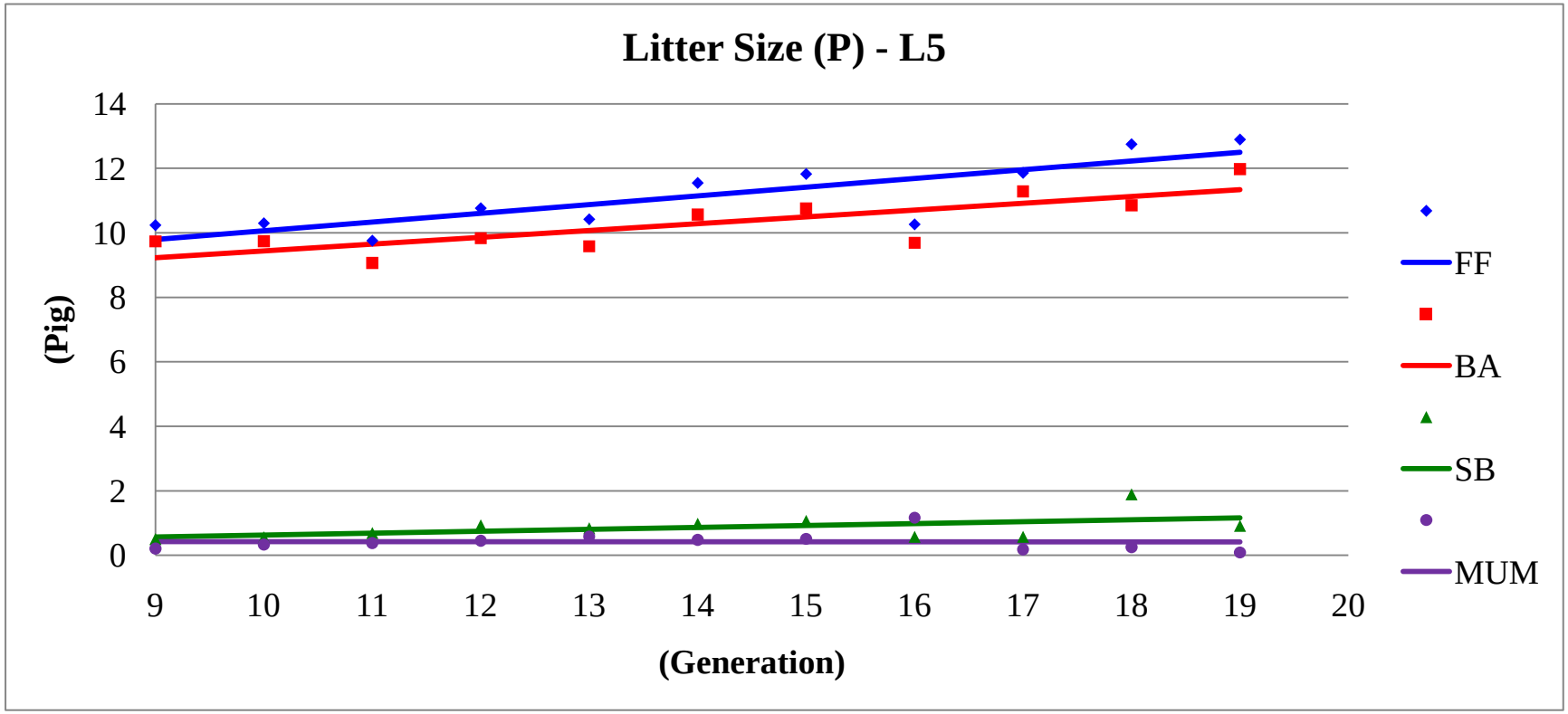

Figure 17.6. **Estimated genetic trends for number of fully form pigs, pigs born alive, stillborn pigs and mummified pigs per litter in selection line 5[a]**

[a] Line:

L5 was selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19.

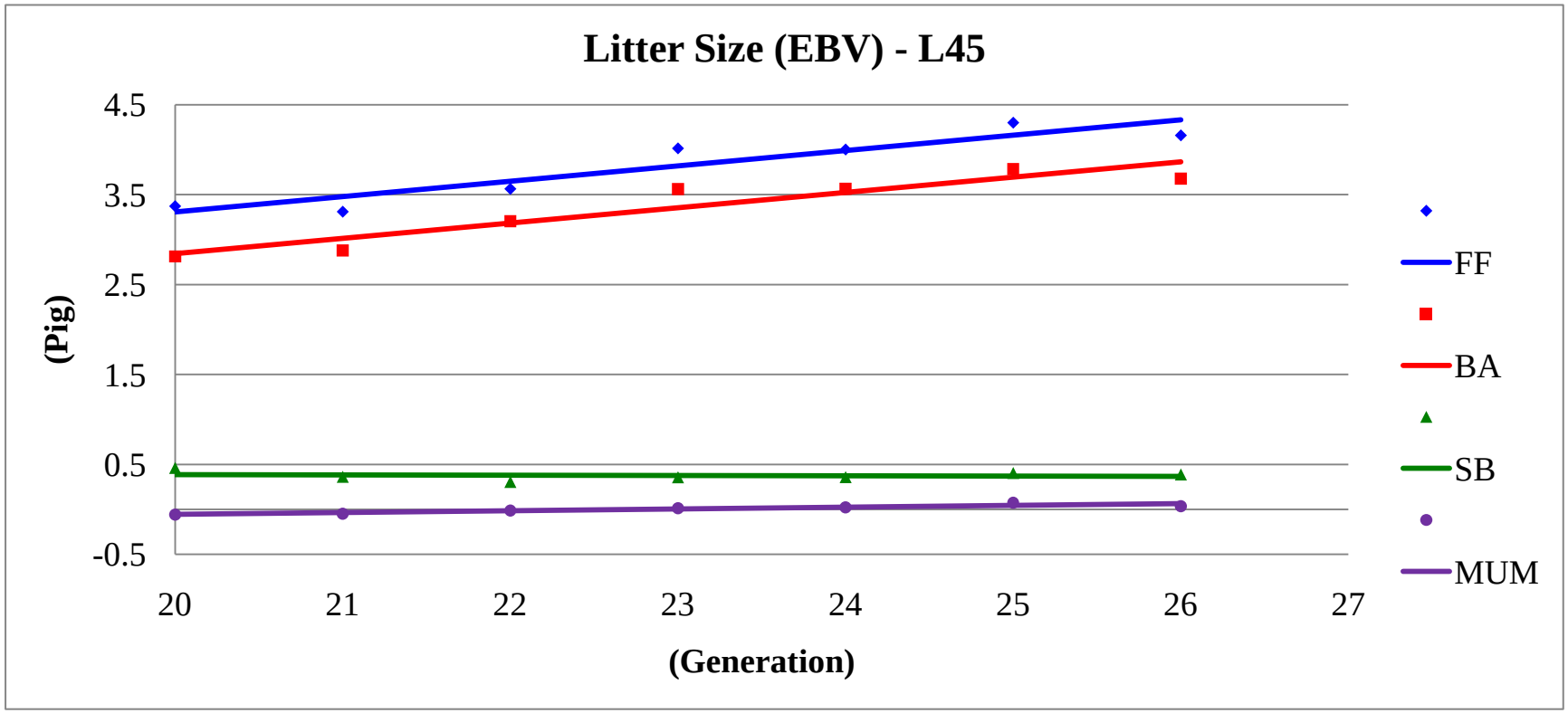

Figure 17.7. **Estimated genetic trends for number of fully form pigs, pigs born alive, stillborn pigs and mummified pigs per litter in selection line 45[a]**

[a] Line:

L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

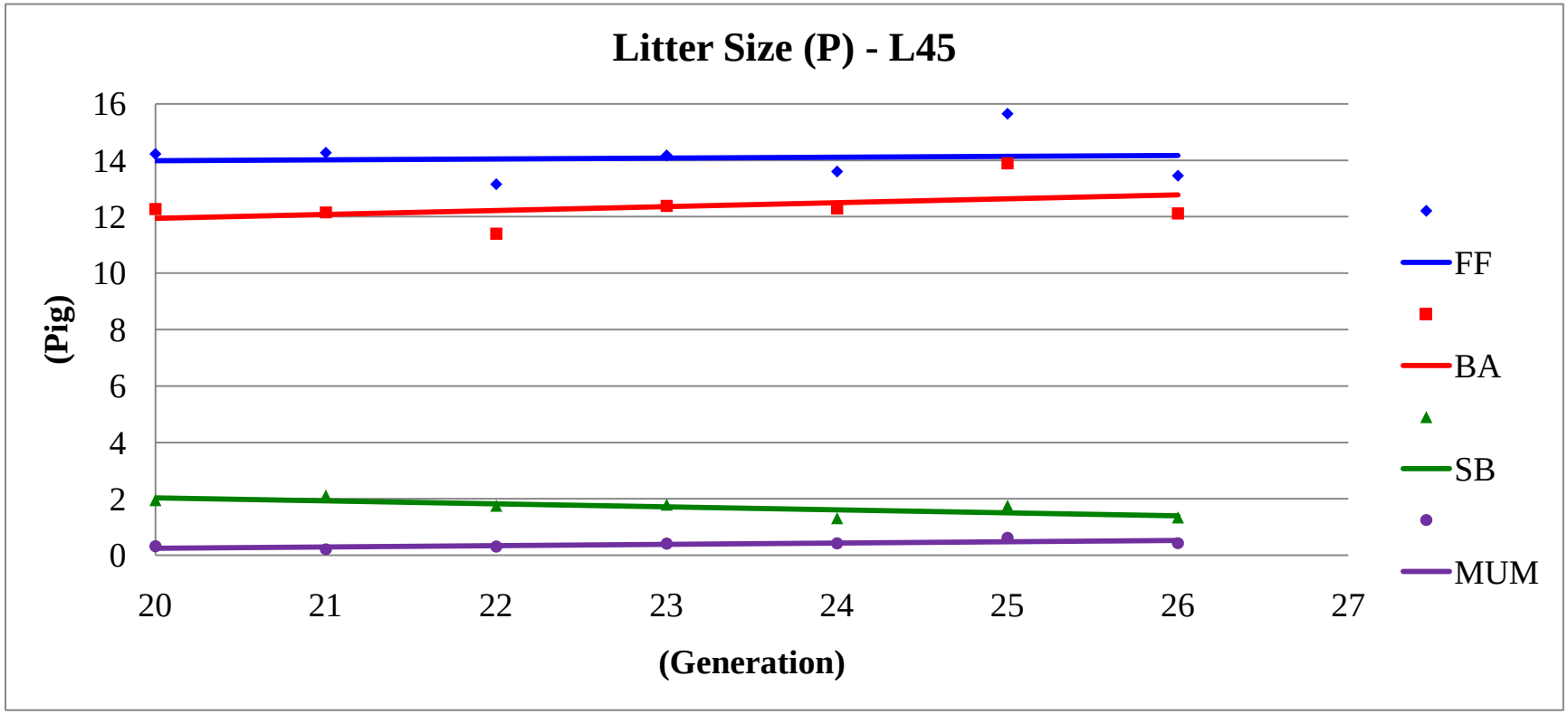

Figure 17.8. **Estimated genetic trends for number of fully form pigs, pigs born alive, stillborn pigs and mummified pigs per litter in selection line 45[a]**

[a] Line:

L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

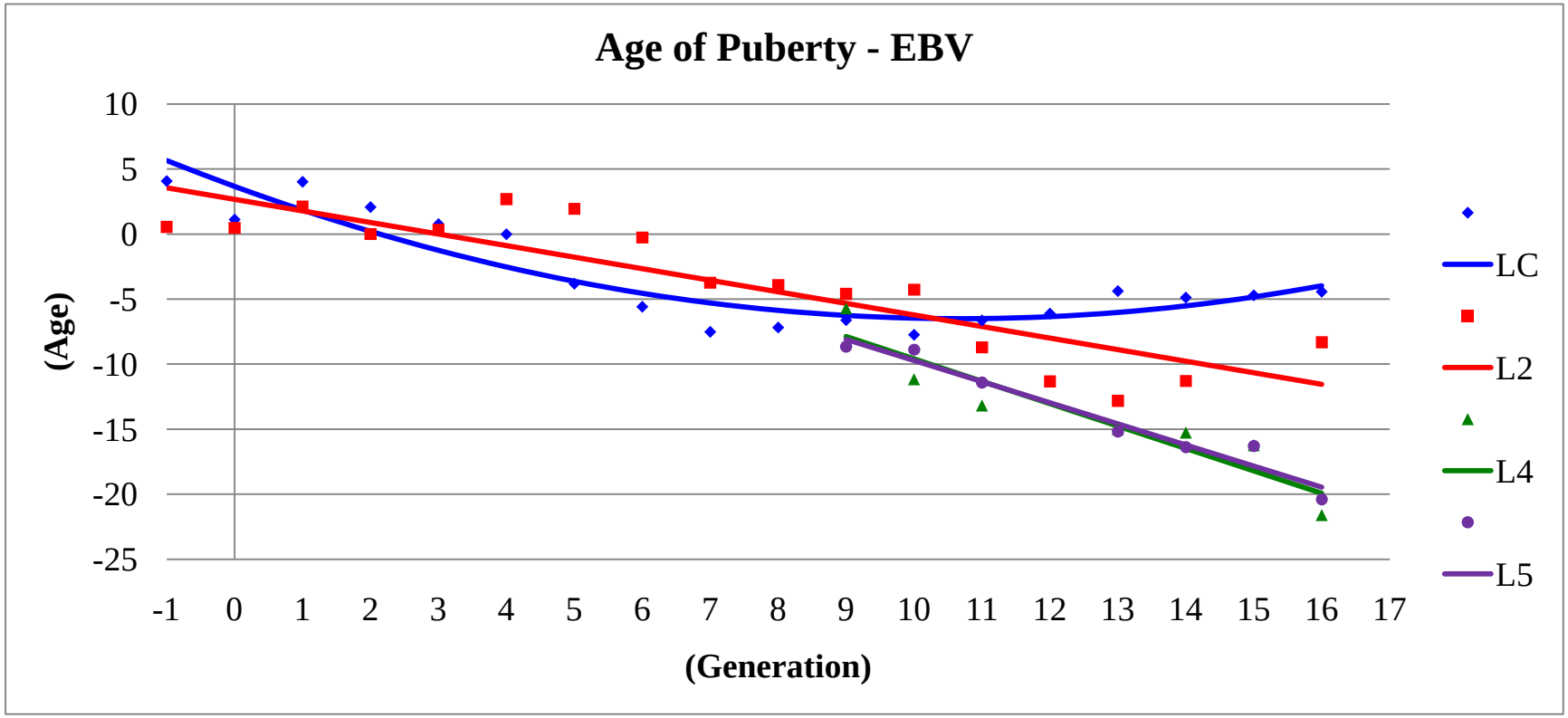

***Figure 18*. Estimated genetic trends for age of puberty by line[a]**

[a] Lines:

LC was a control line in generation 0-16;

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14 and for increased number of born live pigs per litter and increased birth weight in generation 15-19;

L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16.

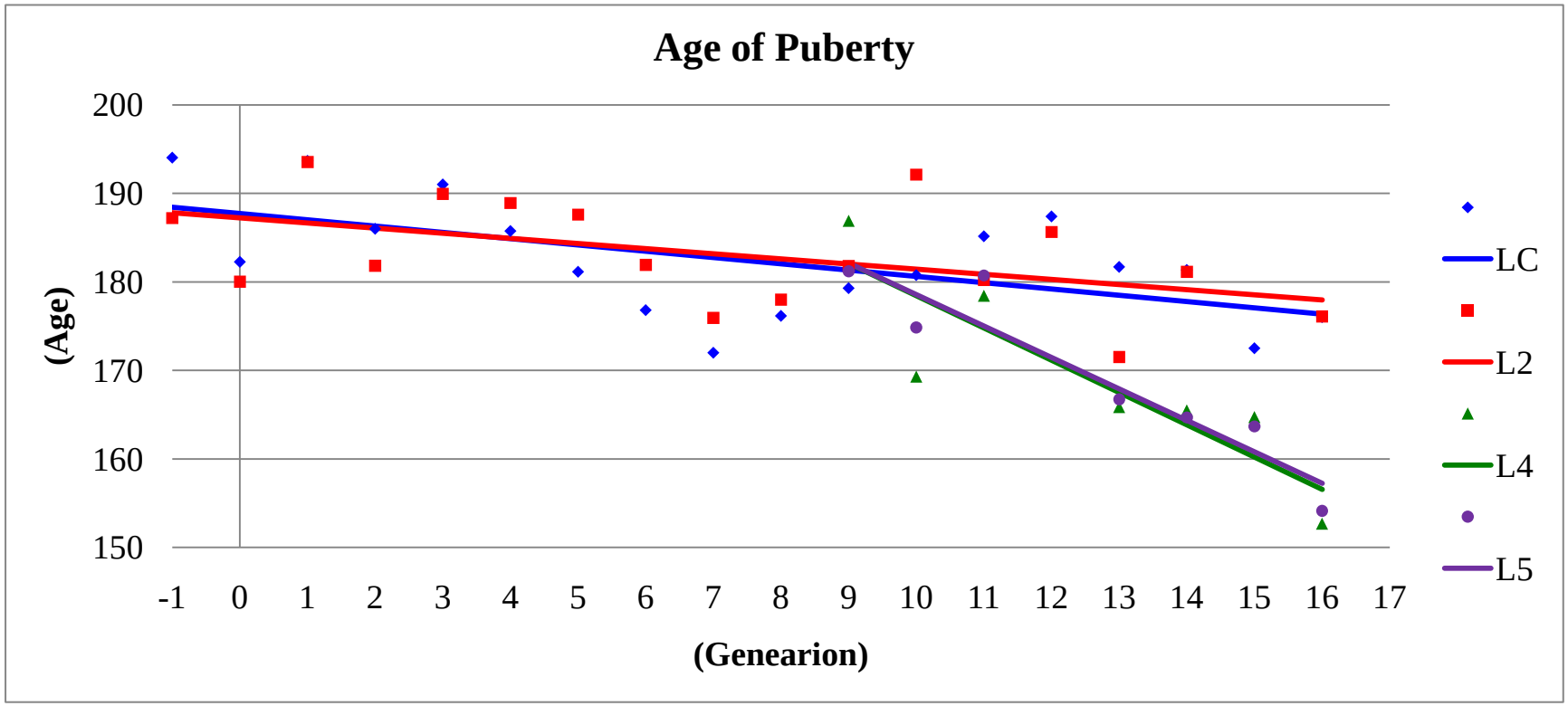

Figure 19. **Estimated phenotypic trends for age of puberty by line[a]**

[a] Lines:

LC was a control line in generation 0-16;

L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14 and for increased number of born live pigs per litter and increased birth weight in generation 15-19;

L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16.

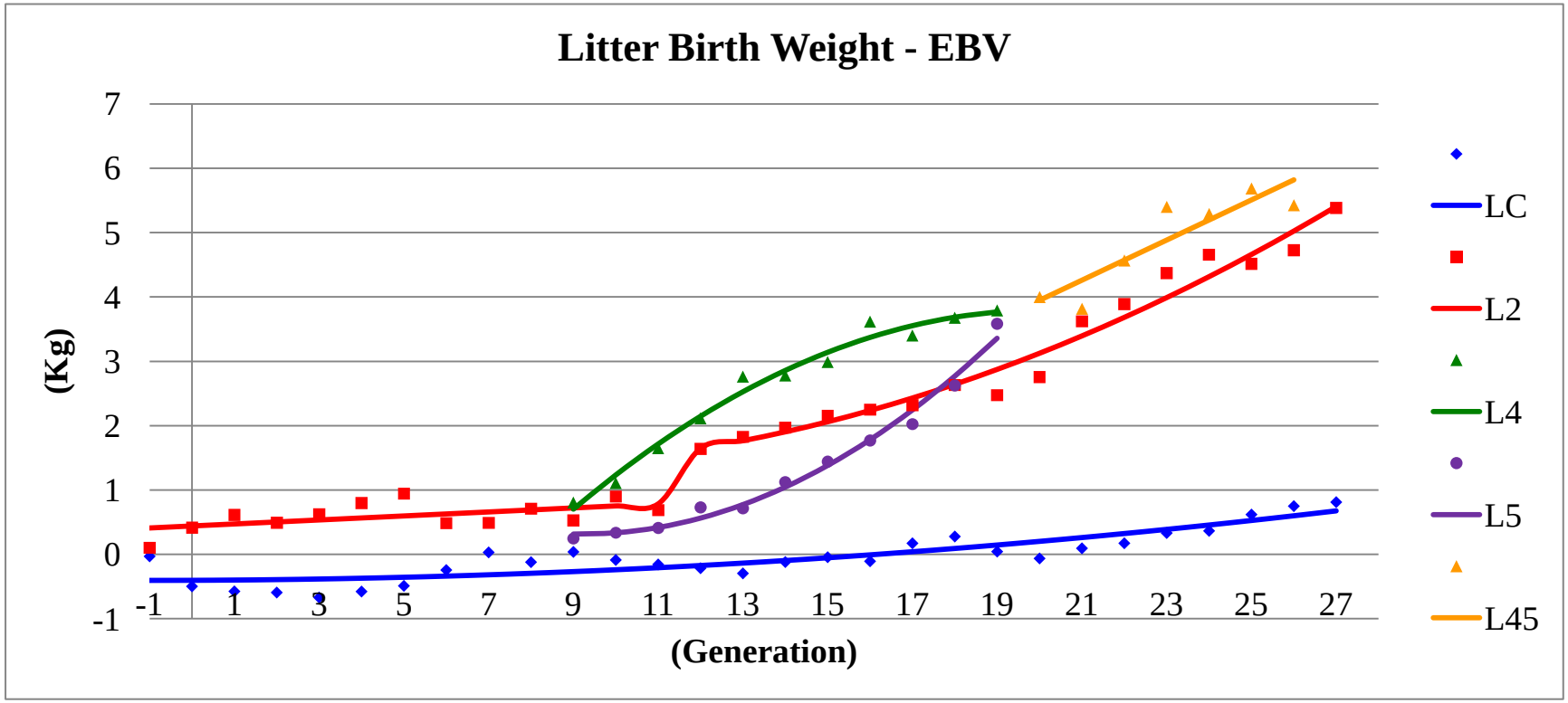

Figure 20. **Estimated genetic trends for litter birth weight by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

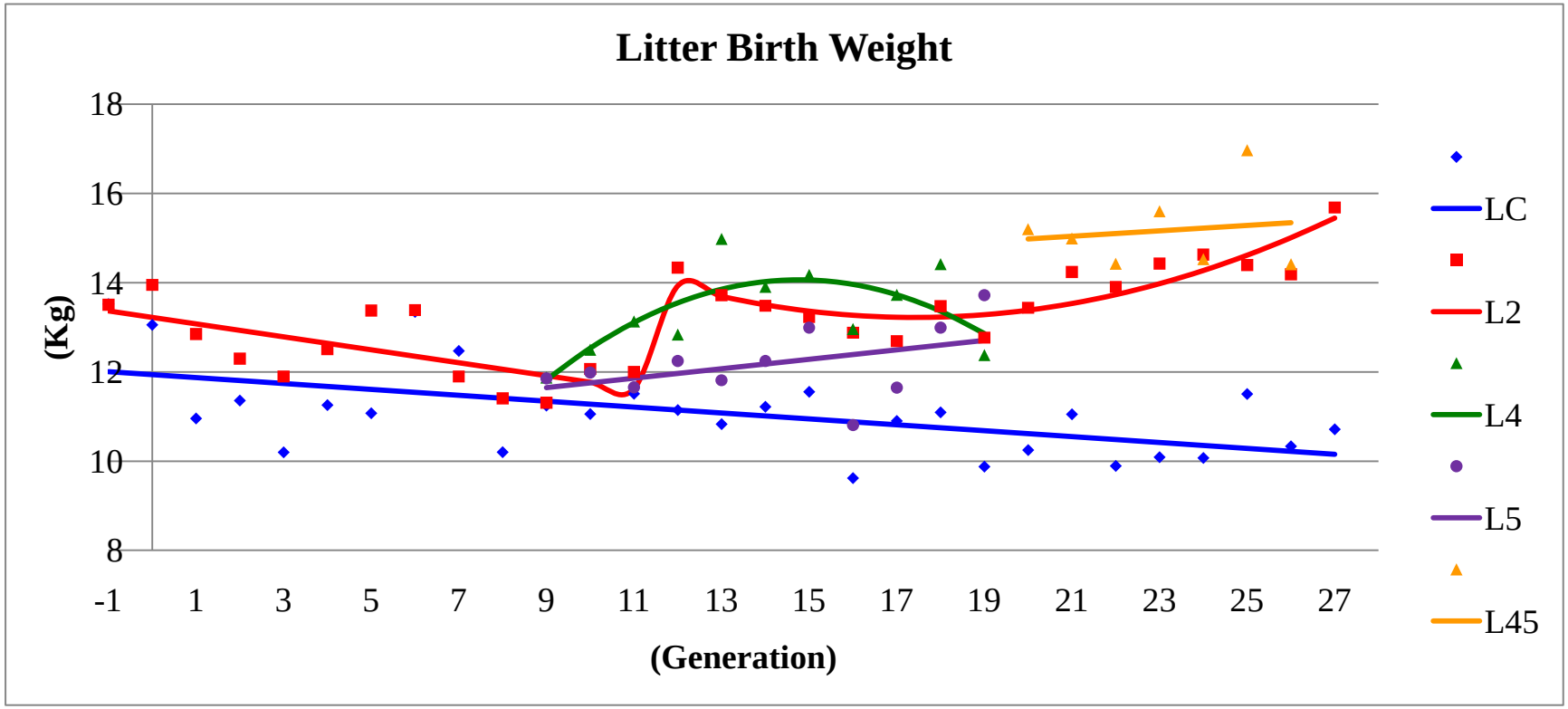

Figure 21. **Estimated phenotypic trends for litter birth weight by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

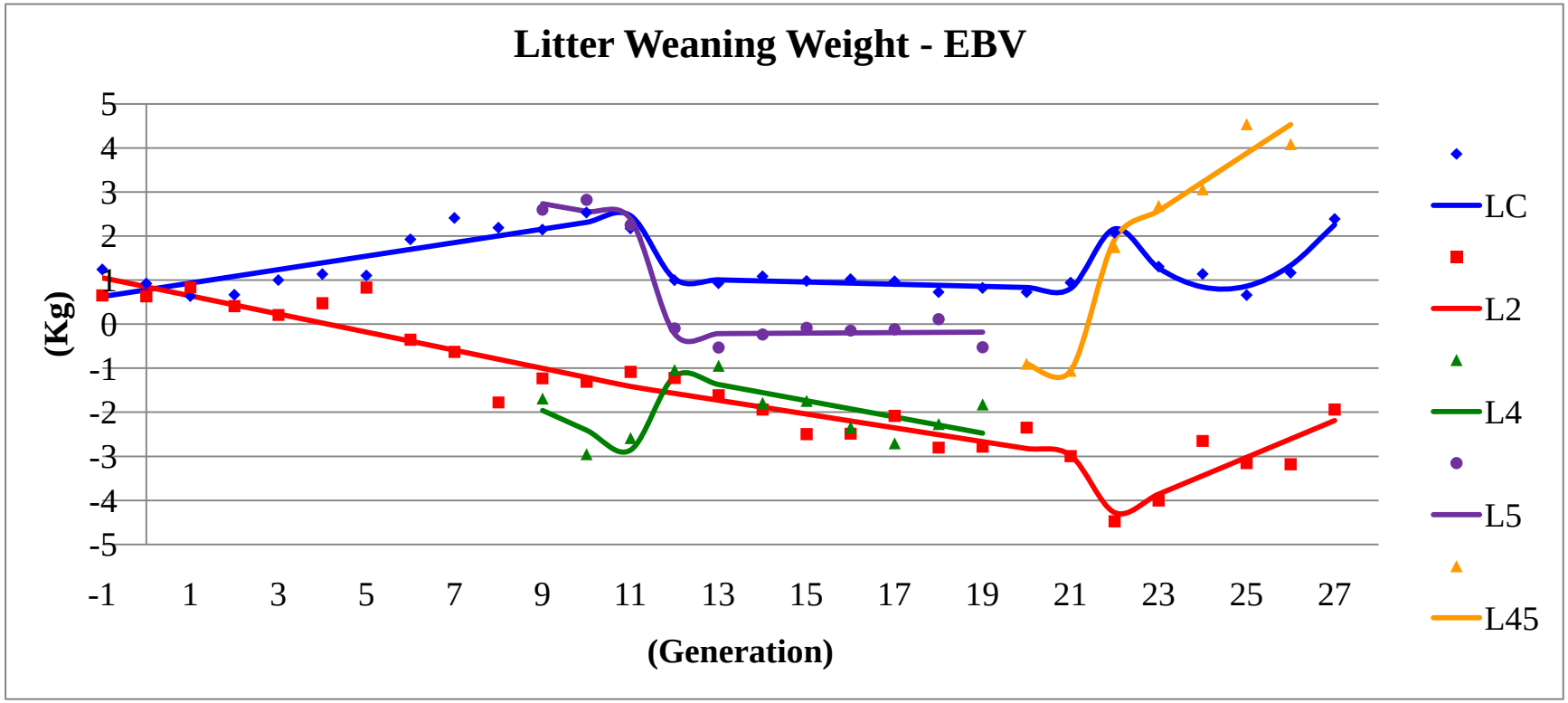

Figure 22. **Estimated genetic trends for litter weaning weight[a] by line[b]**

[a] Litter weaning weight: at 28 days in generations 0-11, at 12 days in generations 12-21 and at 18 days in generations 22-27.

[b] Lines: LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

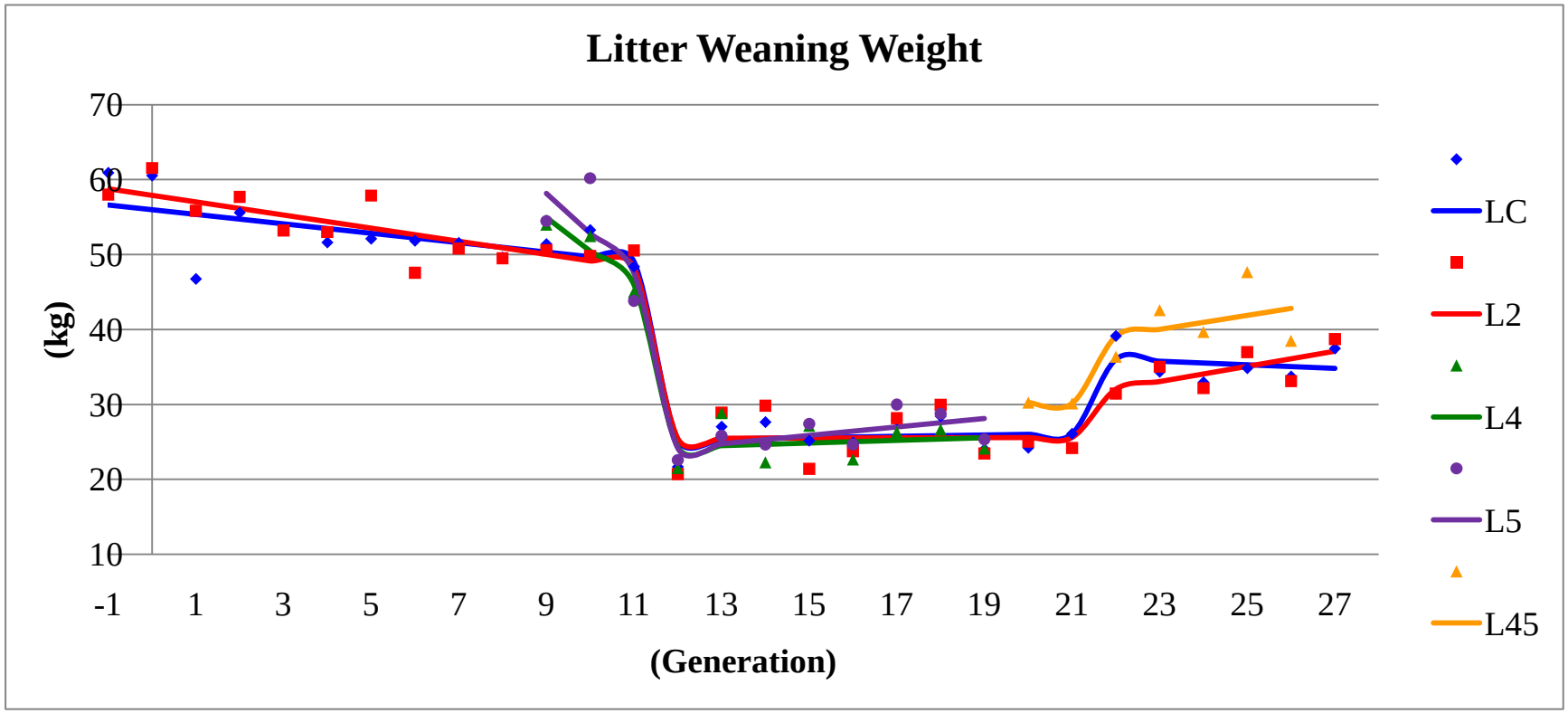

Figure 23. **Estimated phenotypic trends for litter weaning weight by line[a]**

[a] Litter weaning weight: at 28 days in generations 0-11, at 12 days in generations 12-21 and at 18 days in generations 22-27.

[b] Lines: LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

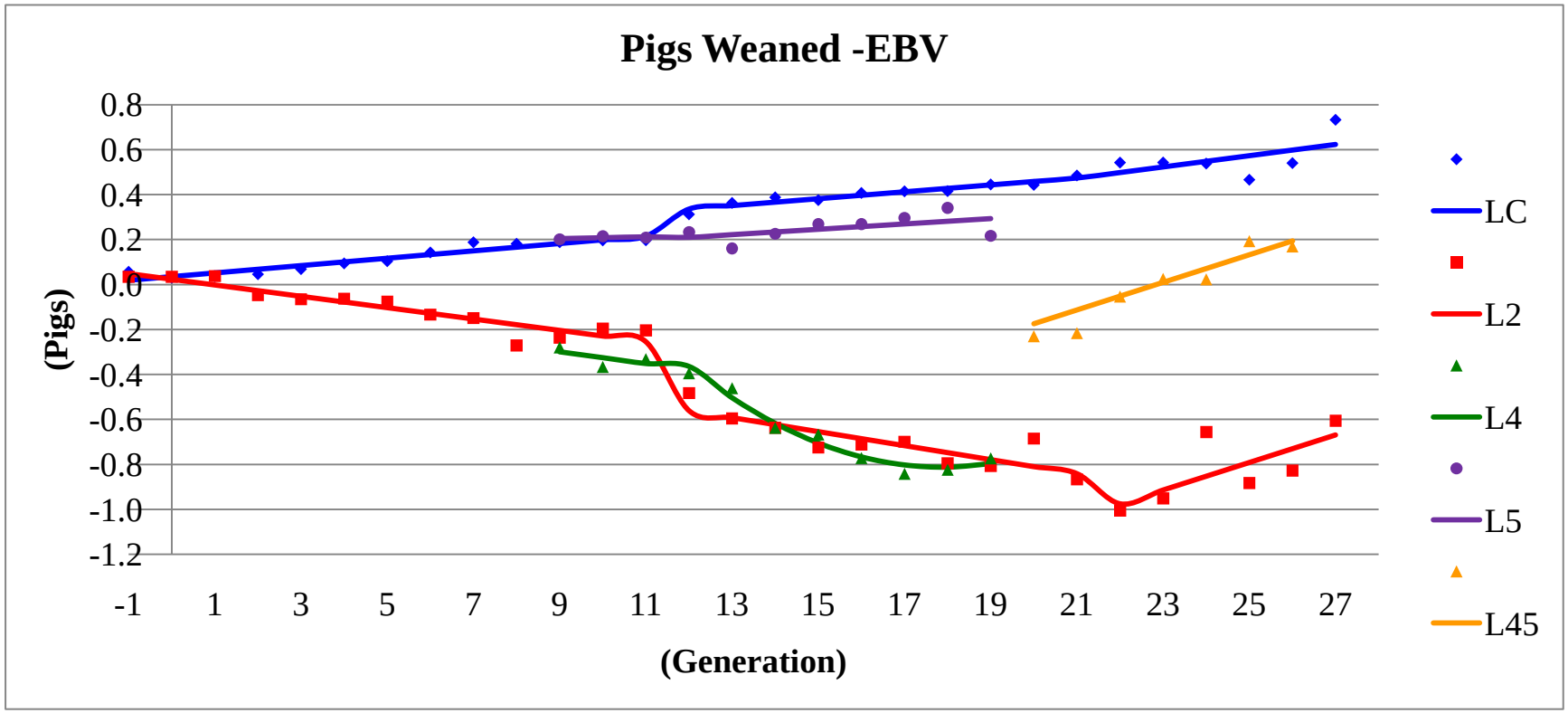

Figure 24. **Estimated genetic trends for number of pigs weaned[a] by line[b]**

[a] Number of weaning pigs: at 28 days in generations 0-11, at 12 days in generations 12-21 and at 18 days in generations 22-27.

[b] Lines: LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

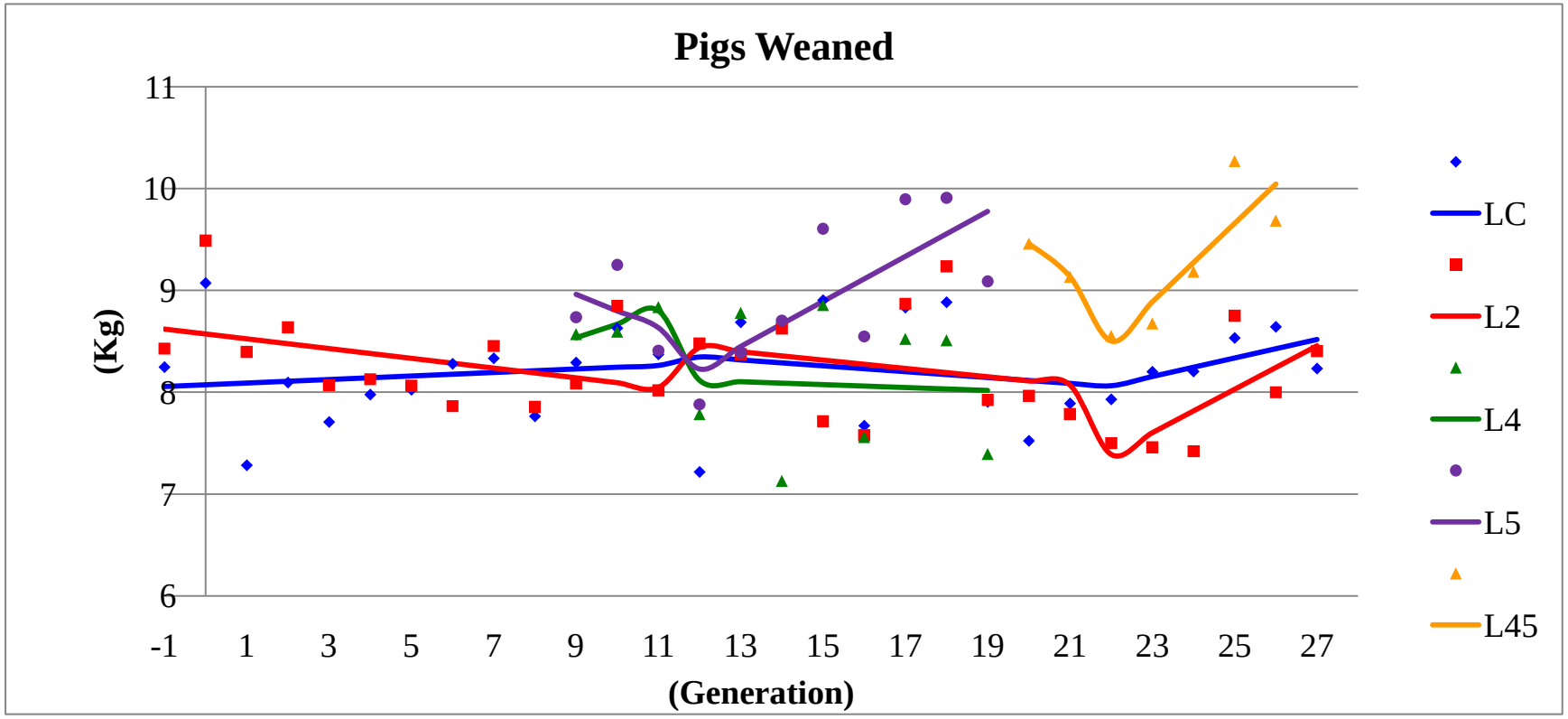

Figure 25. **Estimated phenotypic trends for number of pigs weaned[a] by line[b]**

[a] Number of weaning pigs: at 28 days in generations 0-11, at 12 days in generations 12-21 and at 18 days in generations 22-27.

[b] Lines: LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

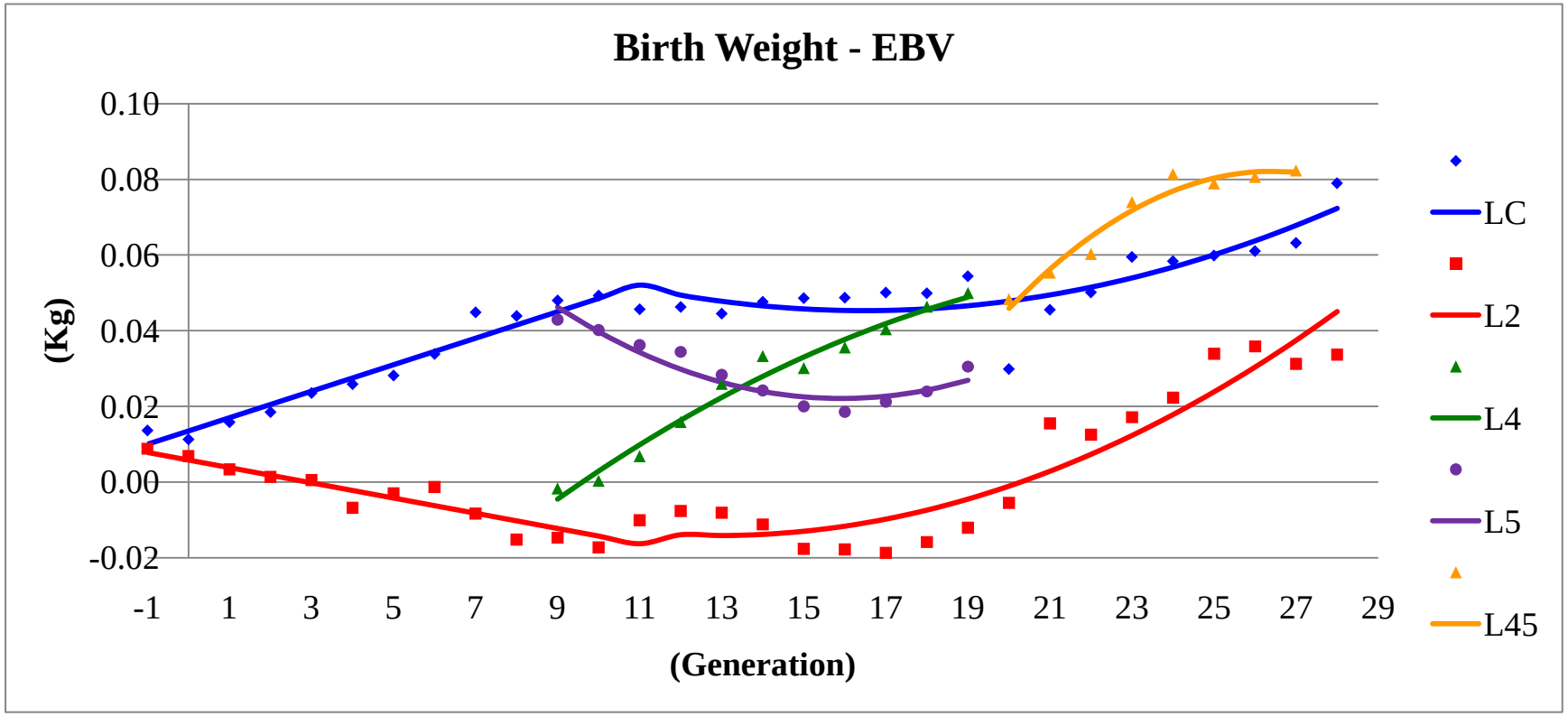

Figure 26. **Estimated genetic trends for birth weight by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

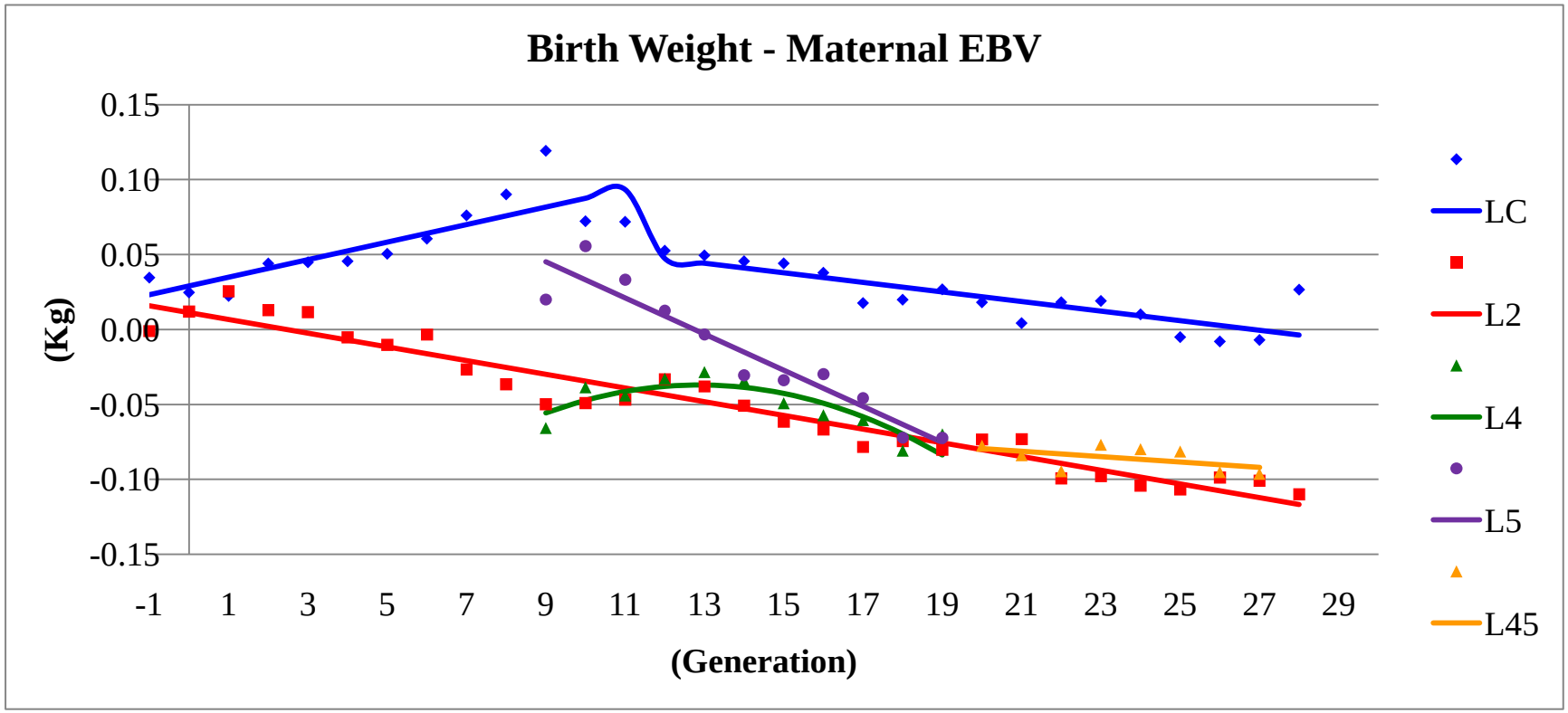

Figure 27. **Estimated maternal genetic trends for birth weight by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

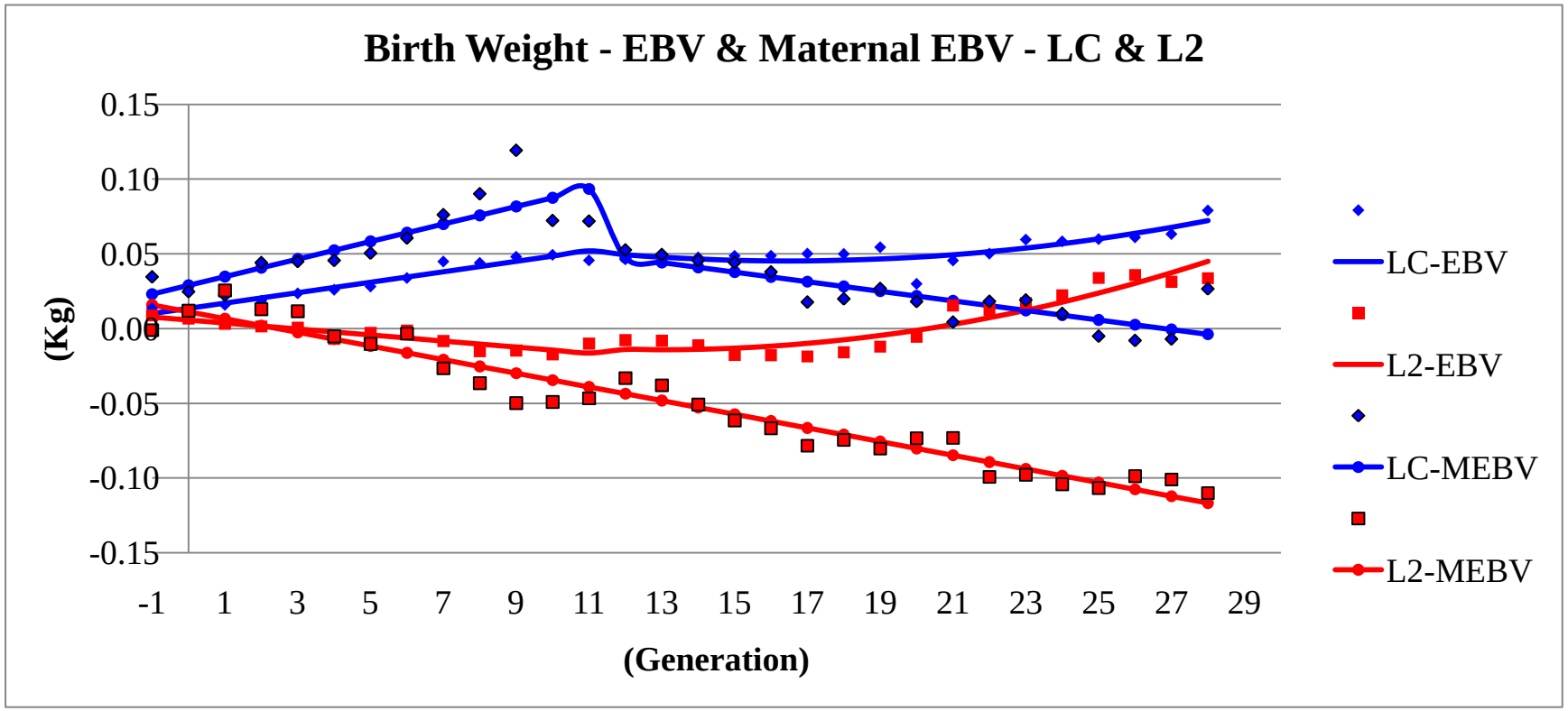

Figure 28.1. **Estimated direct (EBV) and maternal (MEBV) genetic trends for birth weight in lines C and 2[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28.

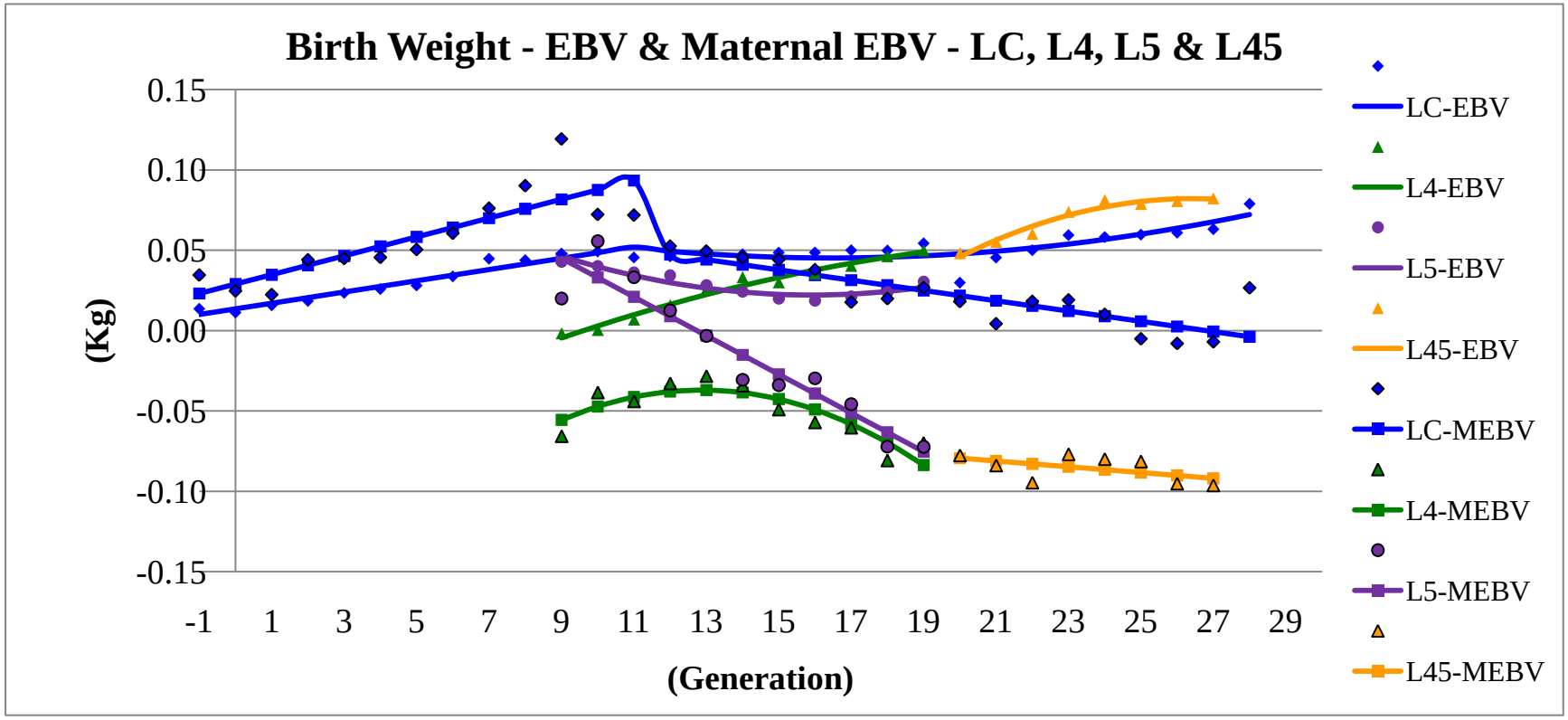

Figure 28.2. **Estimated direct (EBV) and maternal (MEBV) genetic trends for birth weight in lines C, 4, 5 and 45[a]**

[a] Lines:

LC was a control line in generation 0-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

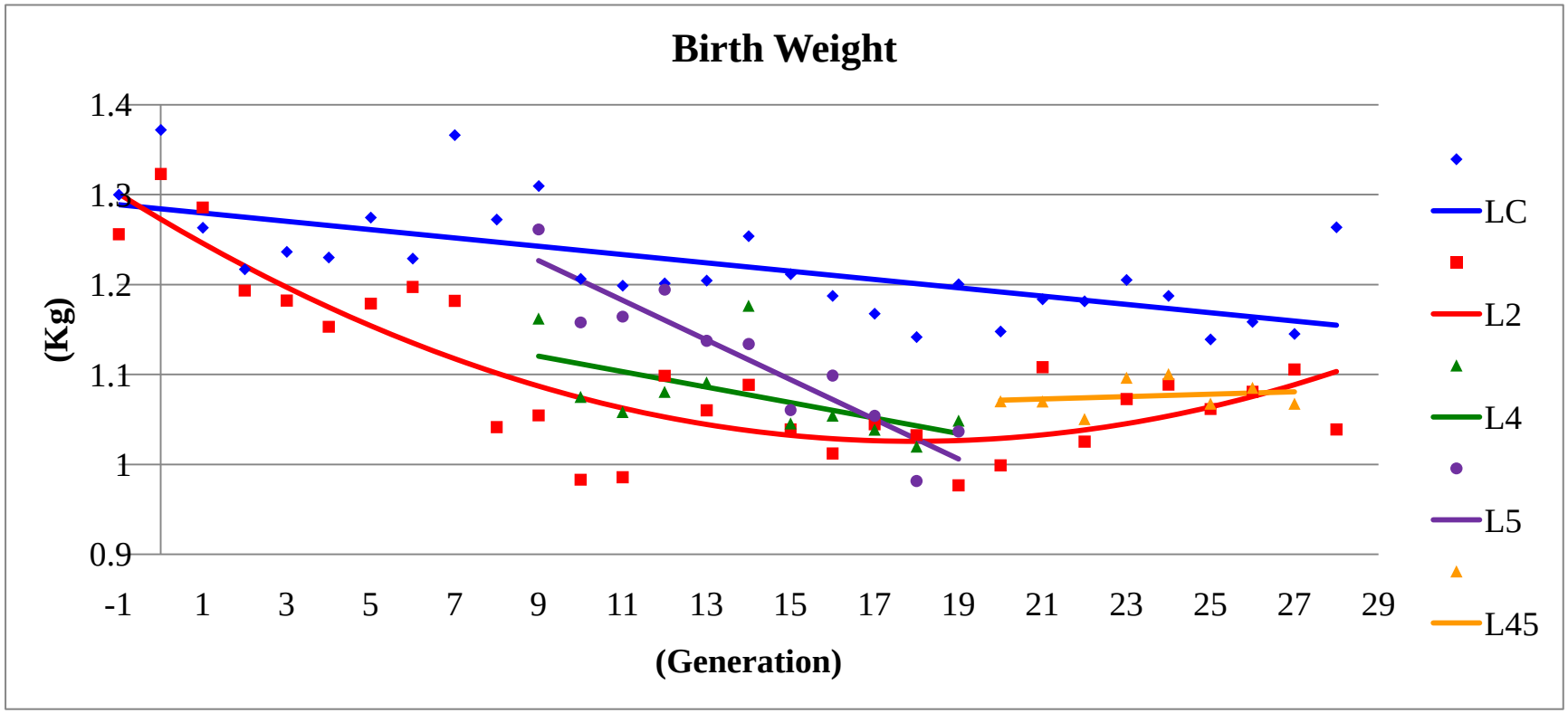

Figure 29. **Estimated phenotypic trends for birth weight by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

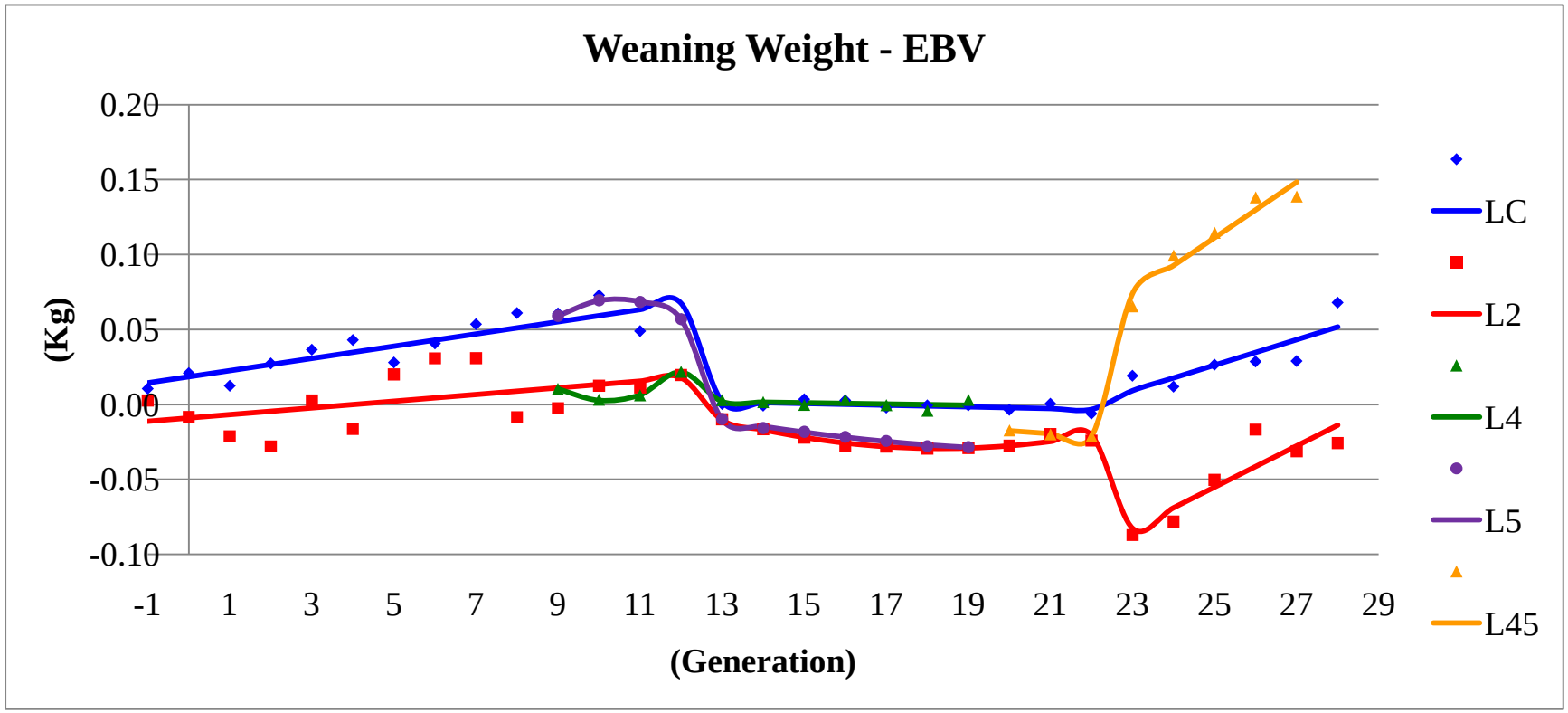

Figure 30. **Estimated genetic trends for weaning weight[a] by line[b]**

[a] Weaning weight at 28 days in generations 0-12, at 12 days in generations 13-22 and at 18 days in generations 23-28.

[b] Lines: LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

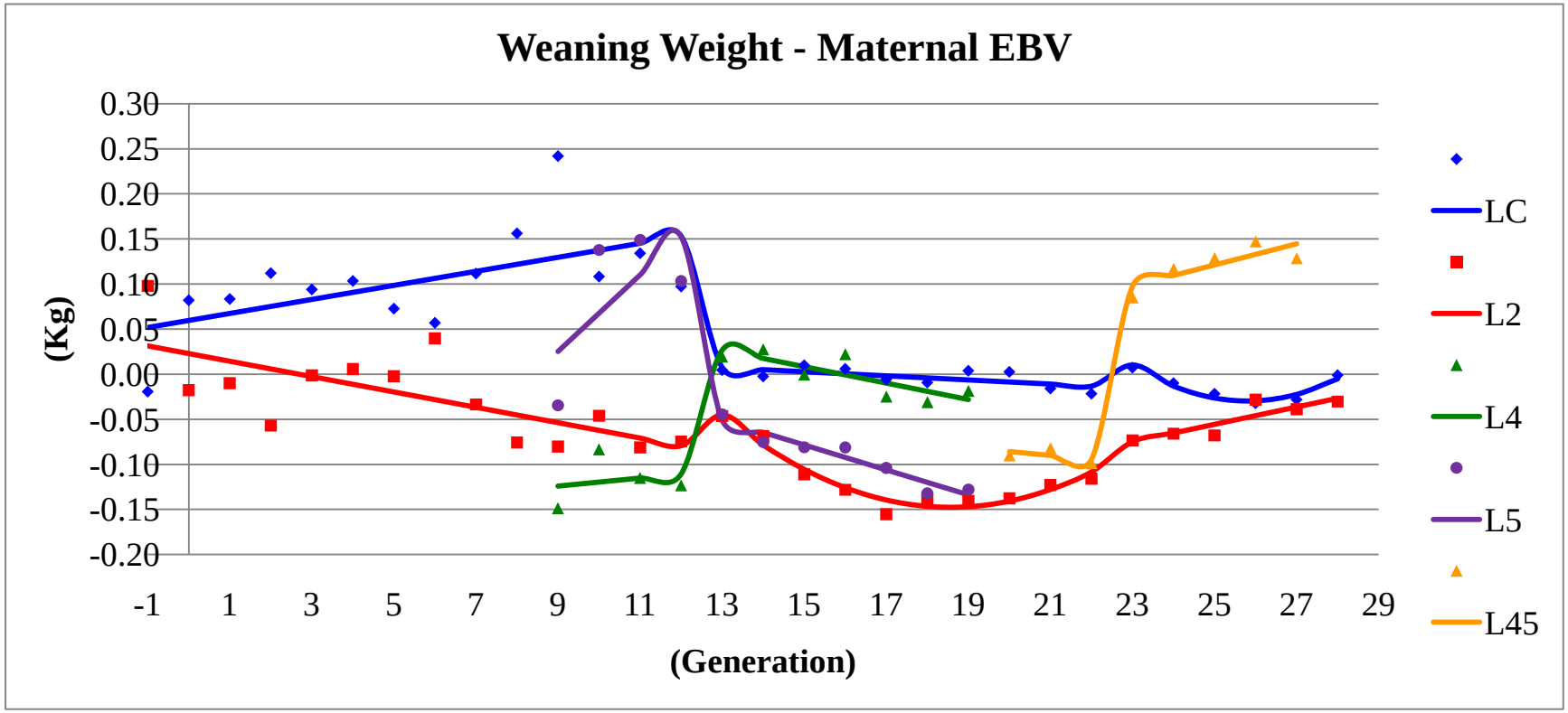

Figure 31. **Estimated maternal genetic trends for weaning weight[a] by line[b]**

[a] Weaning weight at 28 days in generations 0-12, at 12 days in generations 13-22 and at 18 days in generations 23-28.

[b] Lines: LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

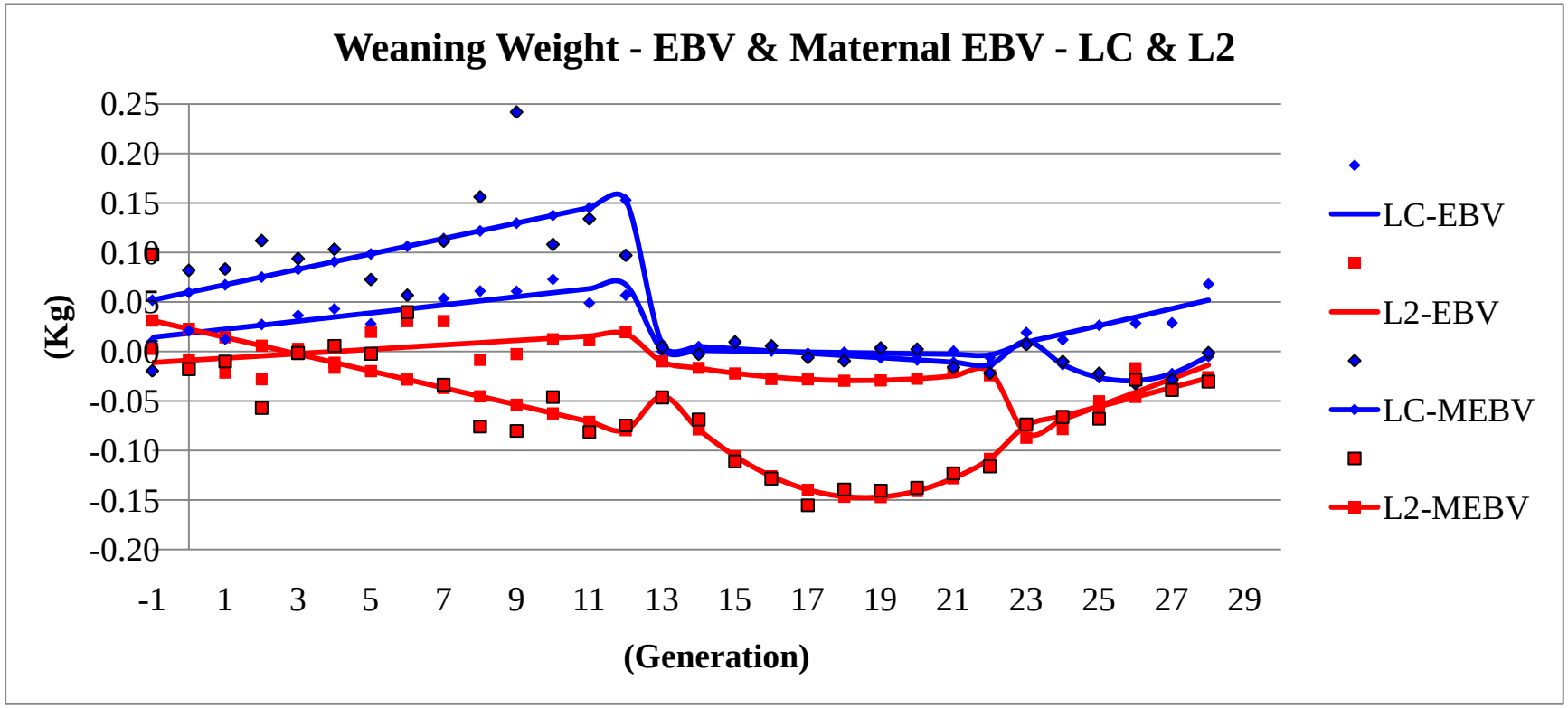

***Figure 32.1*. Estimated direct (EBV) and maternal (MEBV) genetic trends for weaned weighta in lines C and 2[b]**

[a] Weaning weight at 28 days in generations 0-12, at 12 days in generations 13-22 and at 18 days in generations 23-28.

[b] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28.

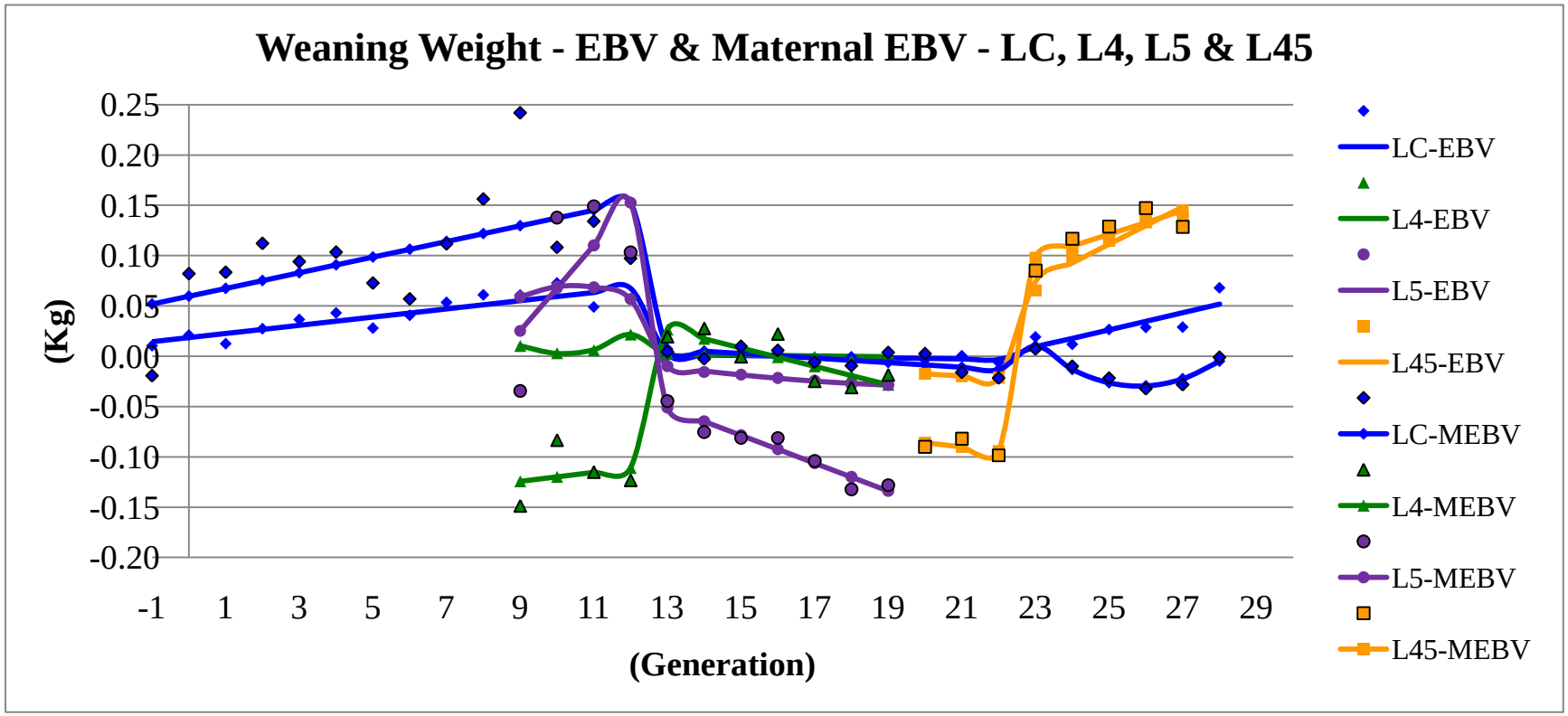

Figure 32.2. **Estimated direct (EBV) and maternal (MEBV) genetic trends for weaned weight[a] in lines C, 4, 5 and 45[b]**

[a] Weaning weight at 28 days in generations 0-12, at 12 days in generations 13-22 and at 18 days in generations 23-28.

[b] Lines: LC was a control line in generation 0-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

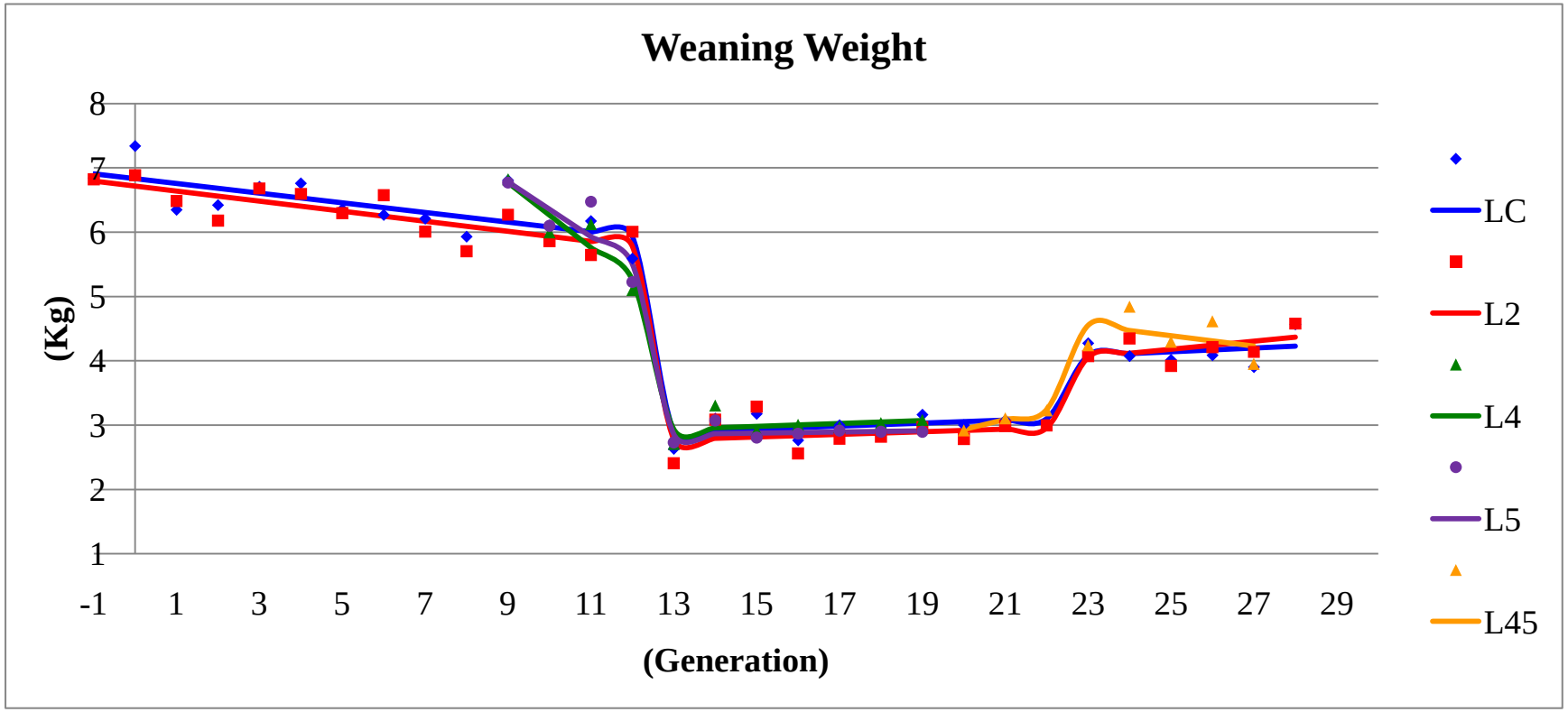

Figure 33. **Estimated phenotypic trends for weaning weight[a] by line[b]**

[a] Weaning weight at 28 days in generations 0-12, at 12 days in generations 13-22 and at 18 days in generations 23-28.

[b] Lines: LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

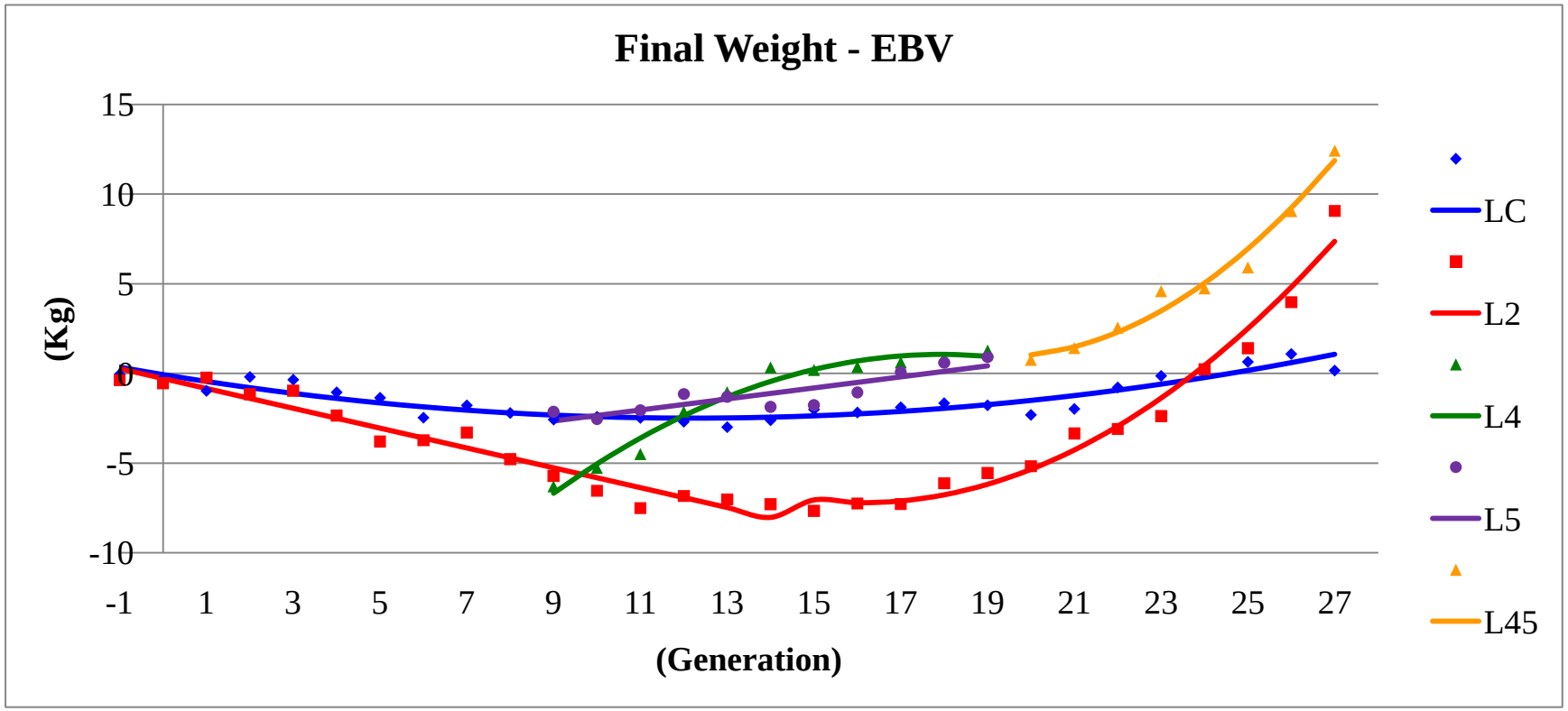

Figure 34. **Estimated genetic trends for final weight by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

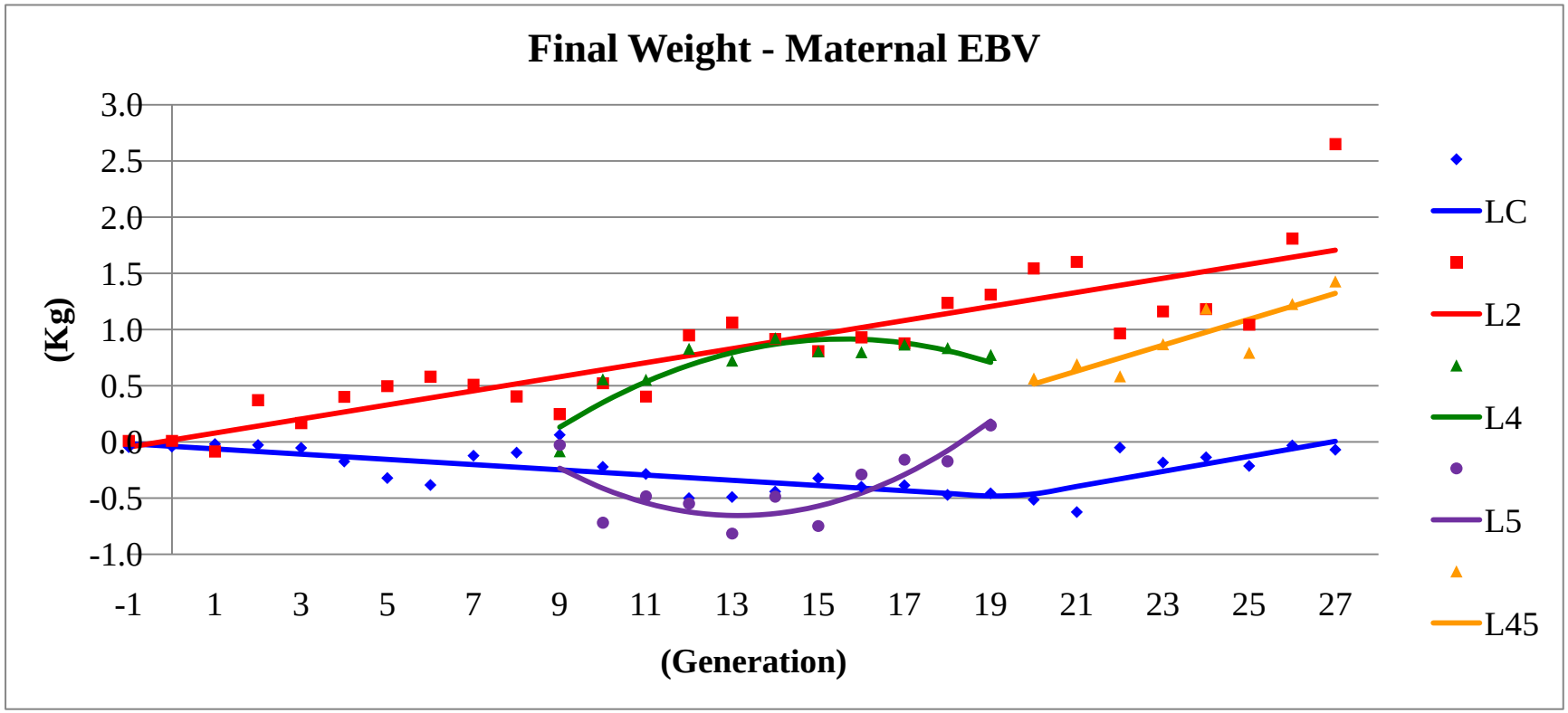

Figure 35. **Estimated maternal genetic trends for final weight by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

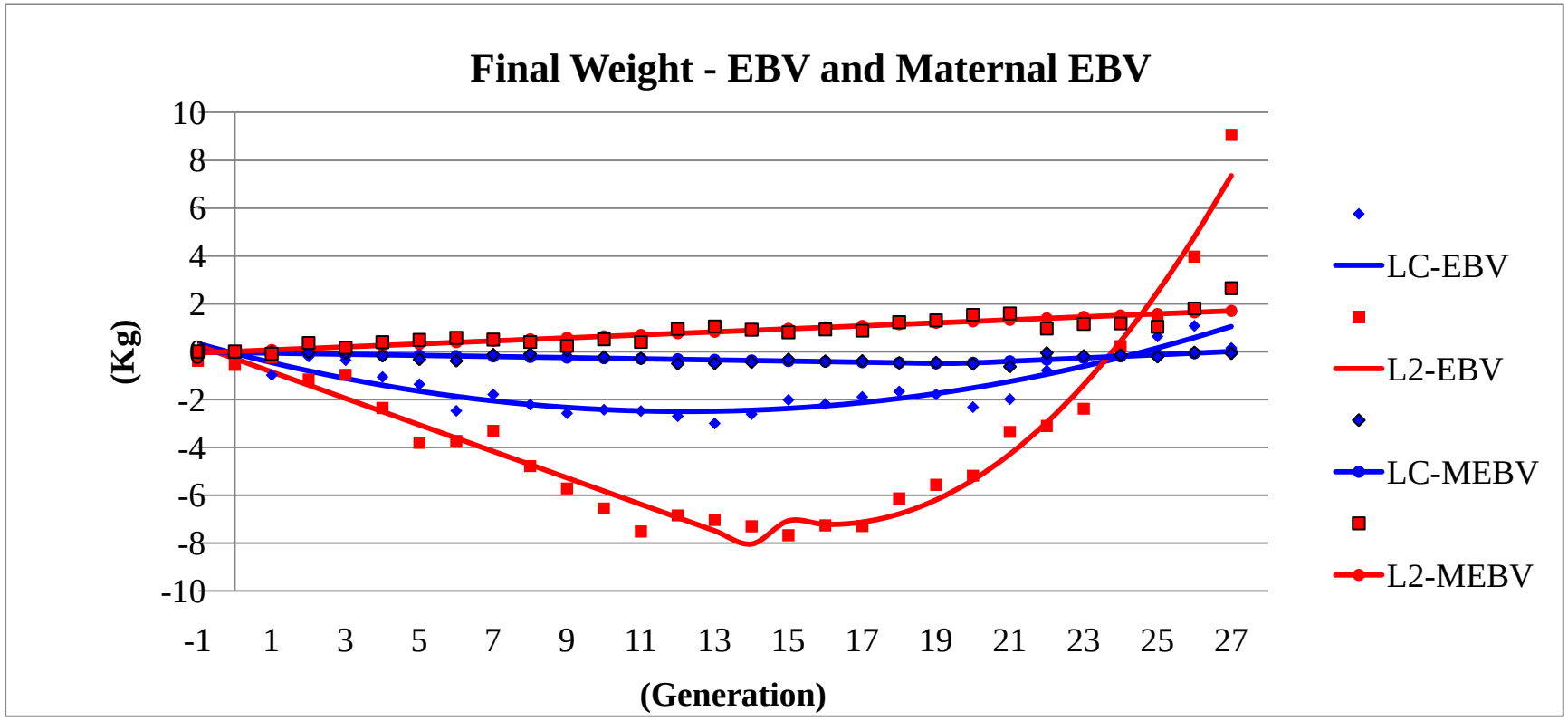

Figure 36.1. **Estimated direct and maternal genetic trends for final weight in lines C and 2[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28.

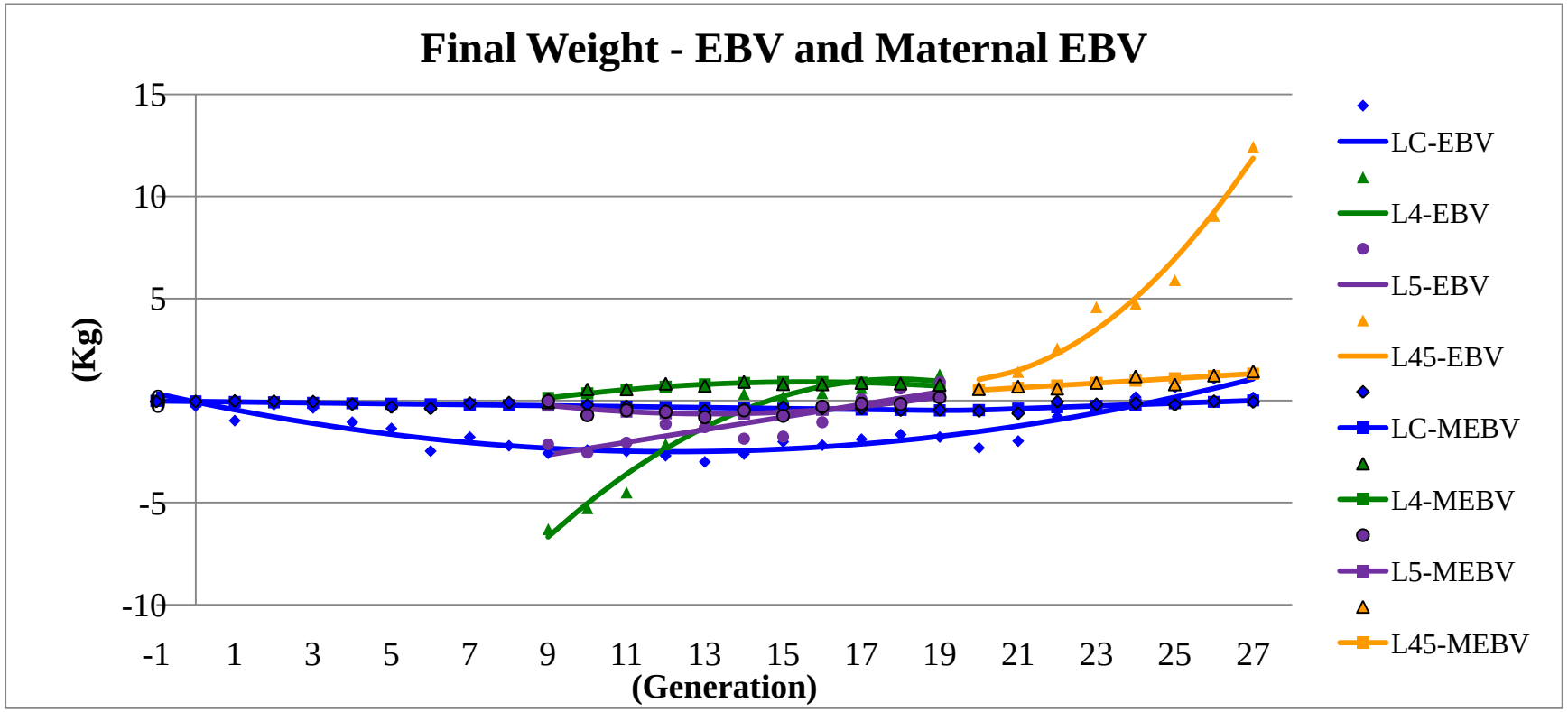

***Figure 36.2*. Estimated direct and maternal genetic trends for final weight in lines C, 4, 5 and 45[a]**

[a] Lines:

LC was a control line in generation 0-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

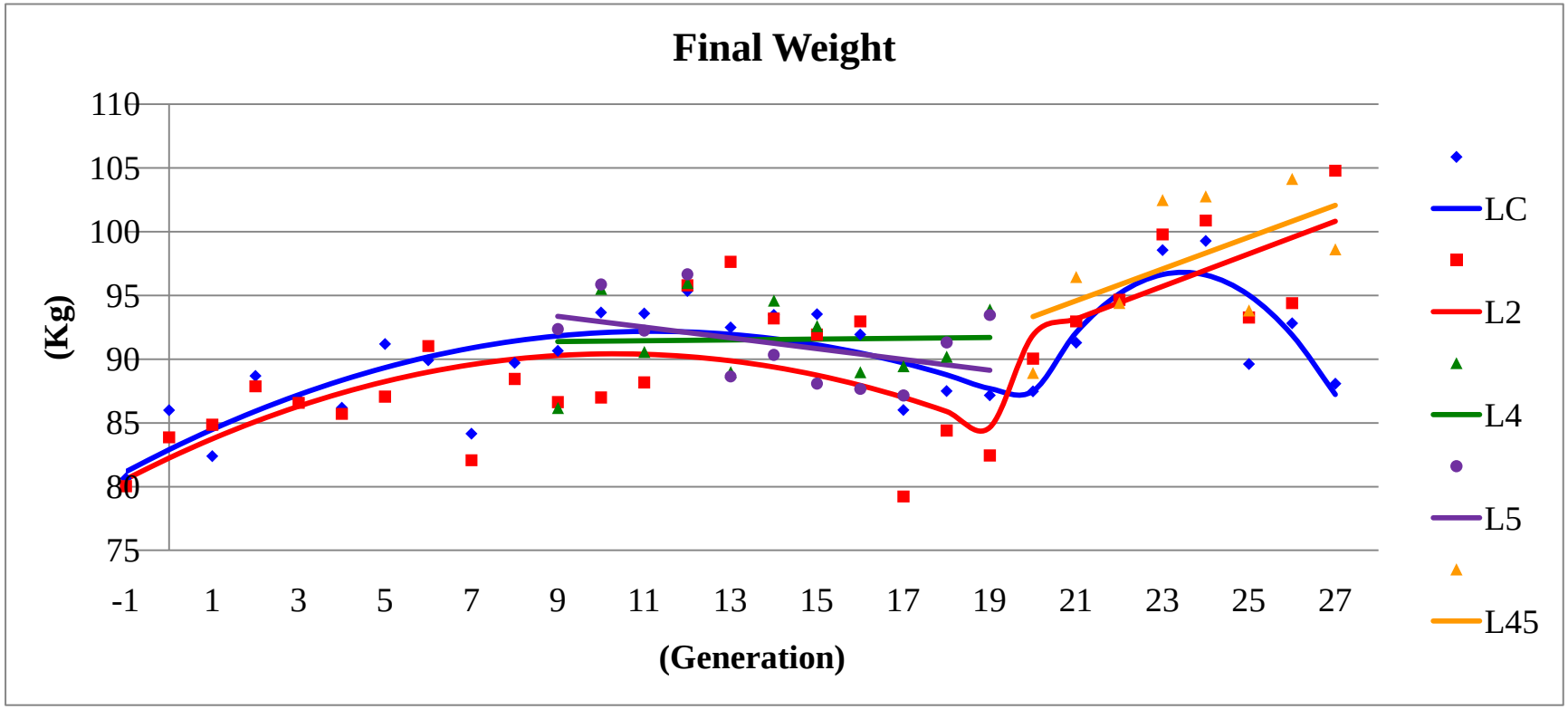

Figure 37. **Estimated phenotypic trends for final weight by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14, for increased number of born live pigs per litter and increased birth weight in generation 15-19 and for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

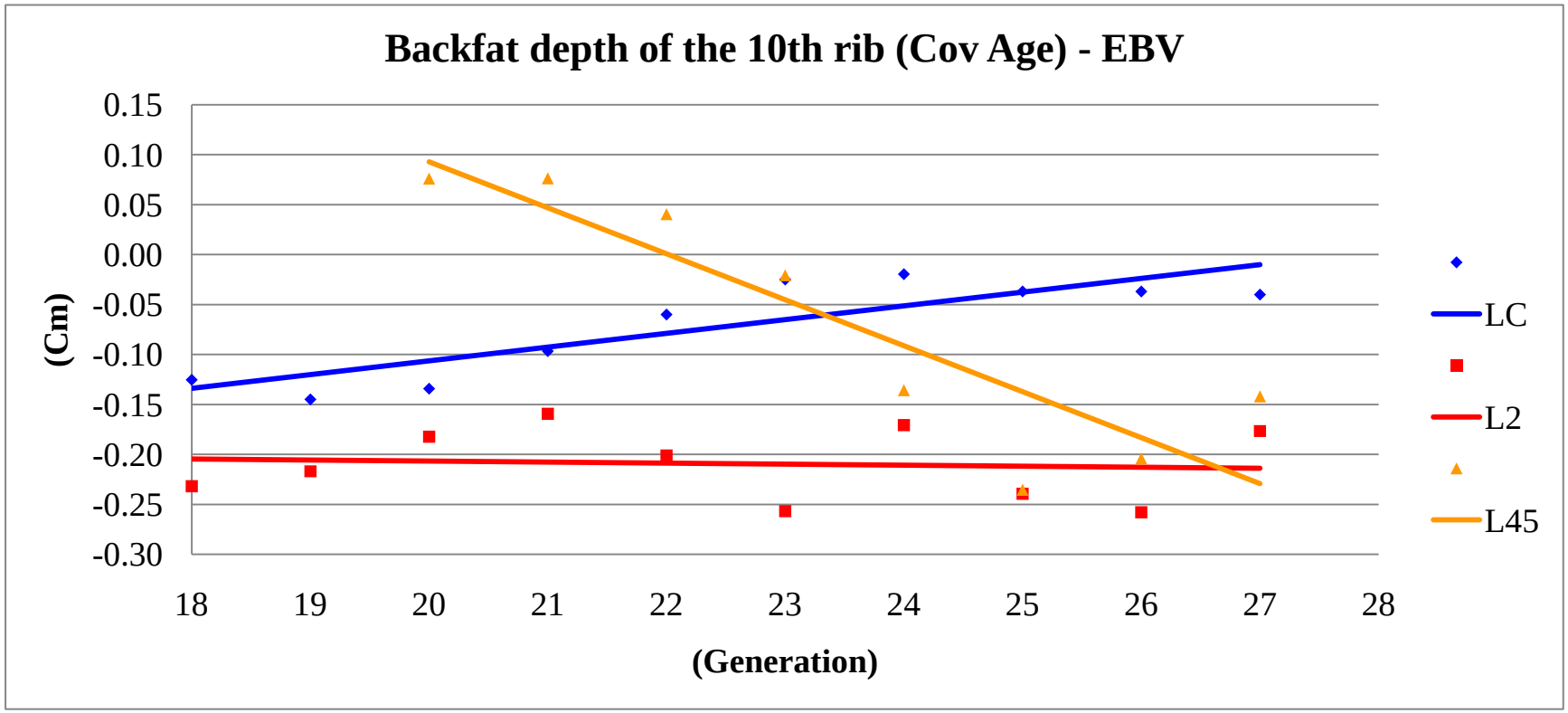

Figure 38. **Estimated genetic trends for backfat depth of the 10th rib with a covariate of age at age of final weight by line[a]**

[a] Lines:

LC was a control line in generation 18-28;

L2 was for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

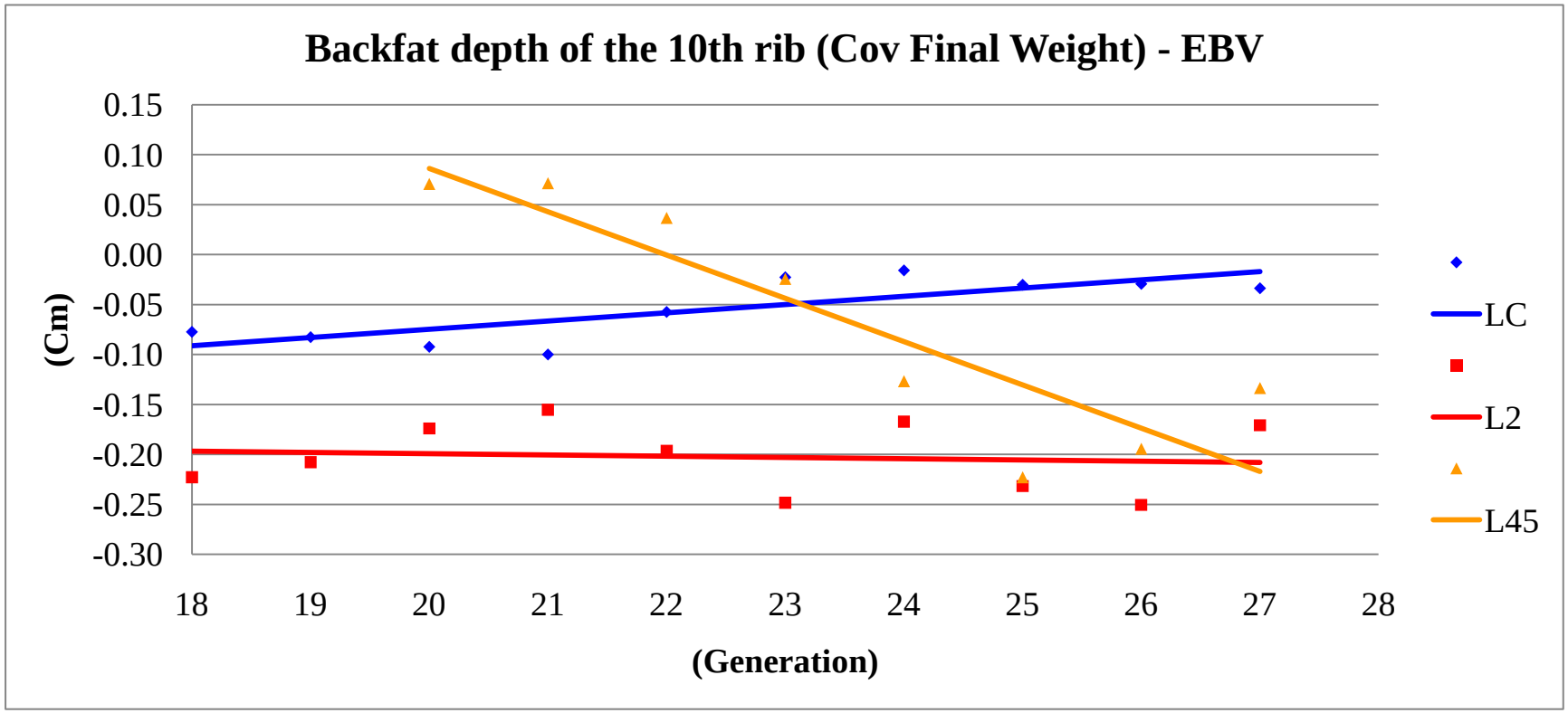

Figure 39. **Estimated genetic trends for backfat depth of the 10th rib with a covariate of final weight at age of final weight by line[a]**

[a] Lines:

LC was a control line in generation 18-28;

L2 was for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

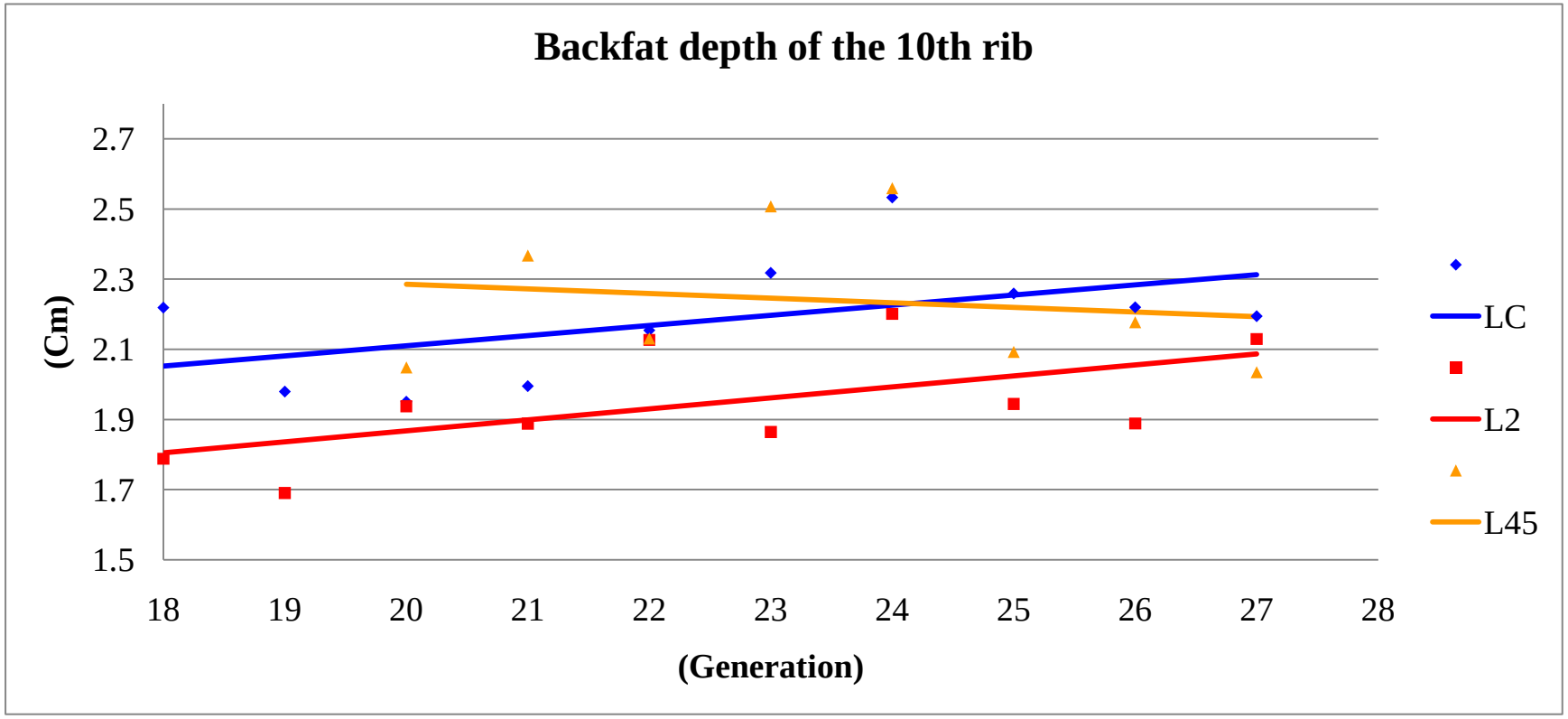

Figure 40. **Estimated phenotypic trends for backfat depth of the 10th rib at age of final weight by line[a]**

[a] Lines:

LC was a control line in generation 18-28;

L2 was for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

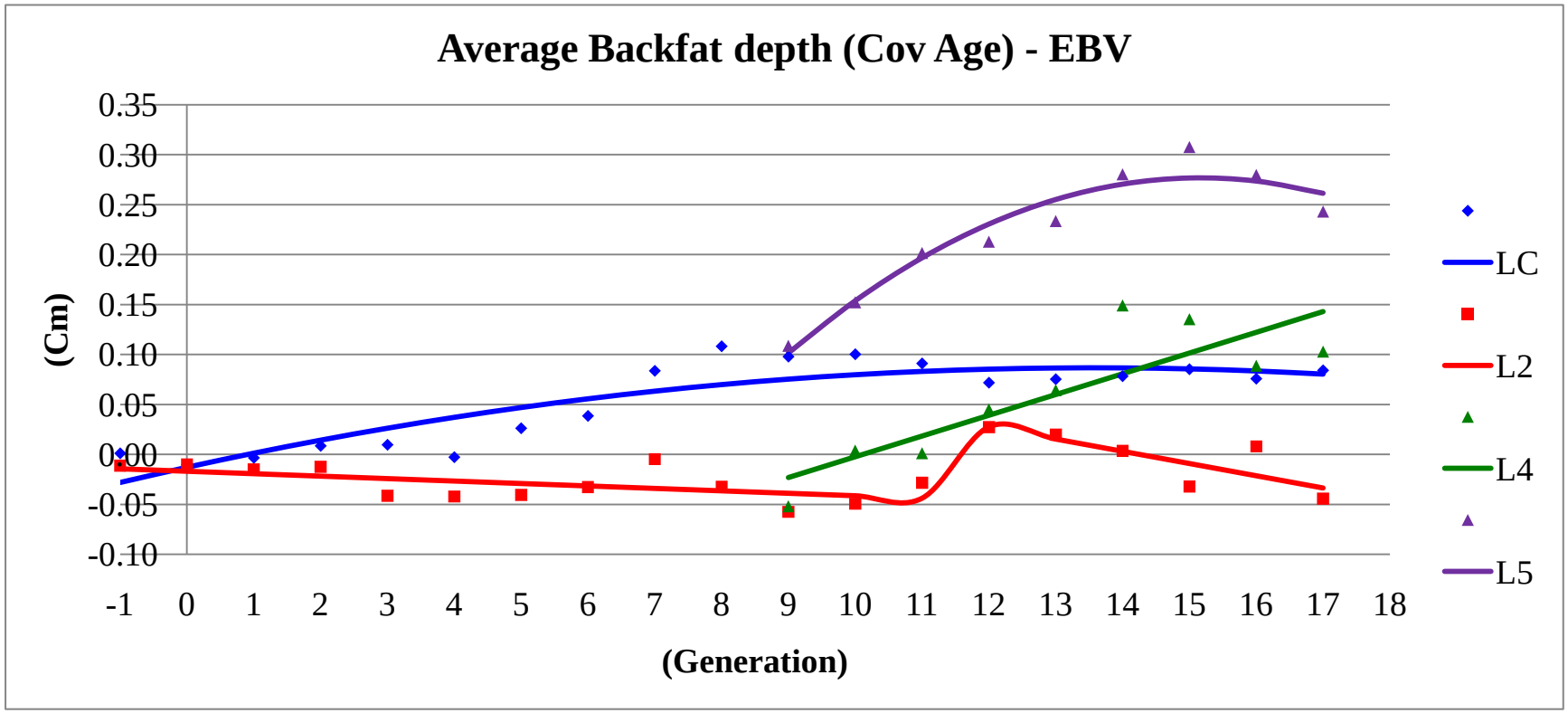

Figure 41. **Estimated genetic trends for average backfat depth with a covariate of age at age of final weight by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14 and for increased number of born live pigs per litter and increased birth weight in generation 15-19; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19.

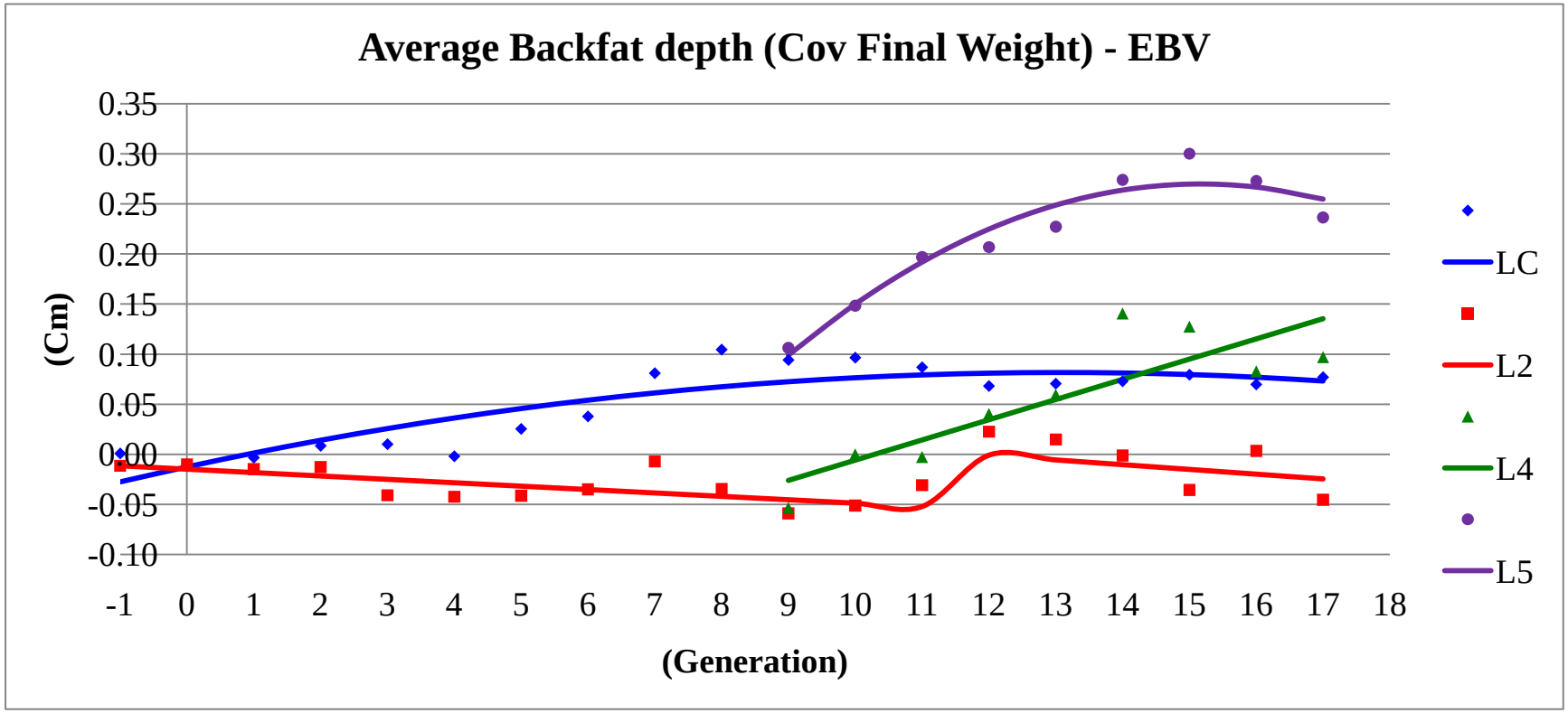

Figure 42. **Estimated genetic trends for average backfat depth with a covariate of final weight at age of final weight by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14 and for increased number of born live pigs per litter and increased birth weight in generation 15-19; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19.

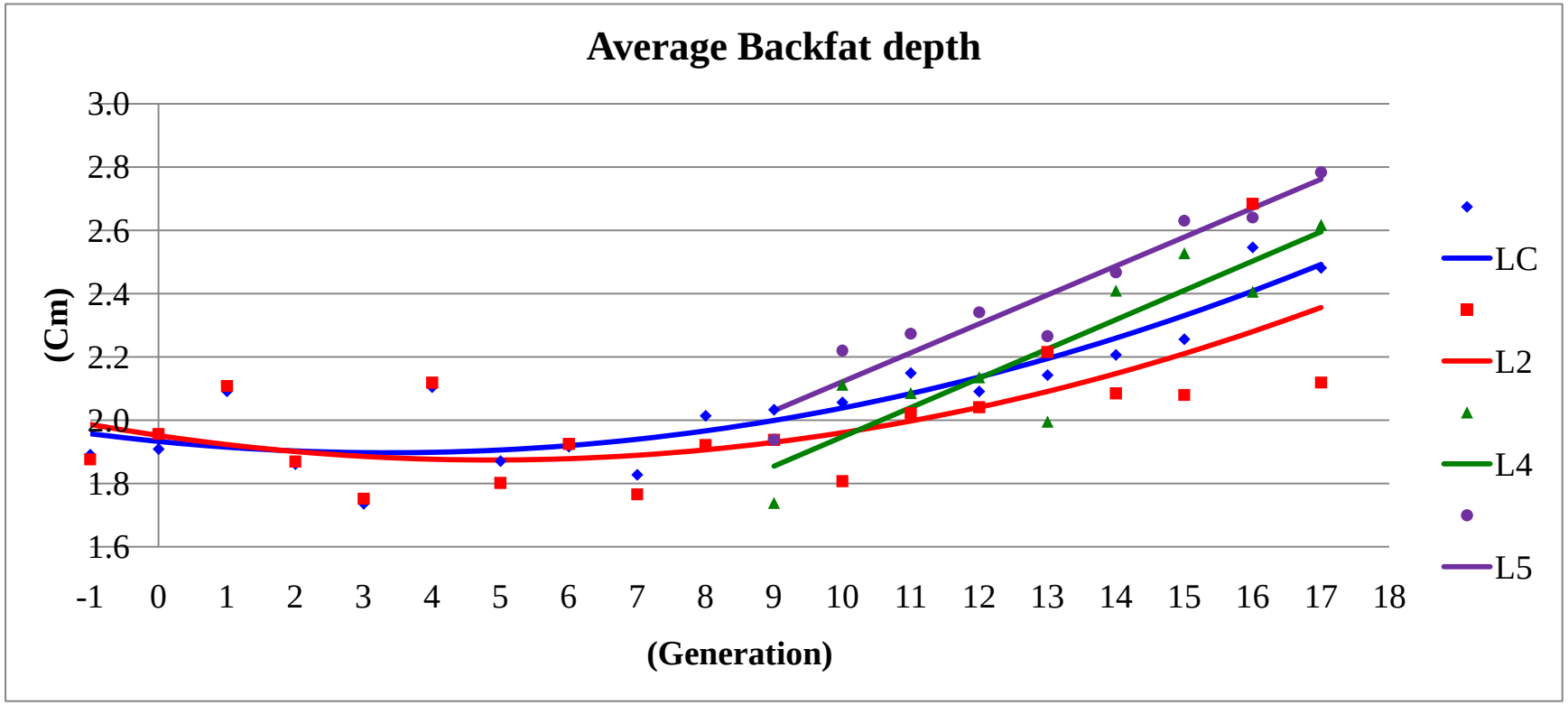

Figure 43. **Estimated phenotypic trends for average backfat depth at age of final weight by line[a]**

[a] Lines:

LC was a control line in generation 0-28; L2 was index selected for increased ovulation rate and embryo survival in generation 0-11, for increased number of fully formed pigs per litter in generation 12-14 and for increased number of born live pigs per litter and increased birth weight in generation 15-19; L4 and L5 were selected in two stages for increased ovulation rate and litter size in generation 8-16 and selected for increased number of born live pigs per litter and increased birth weight in generations 17 – 19.

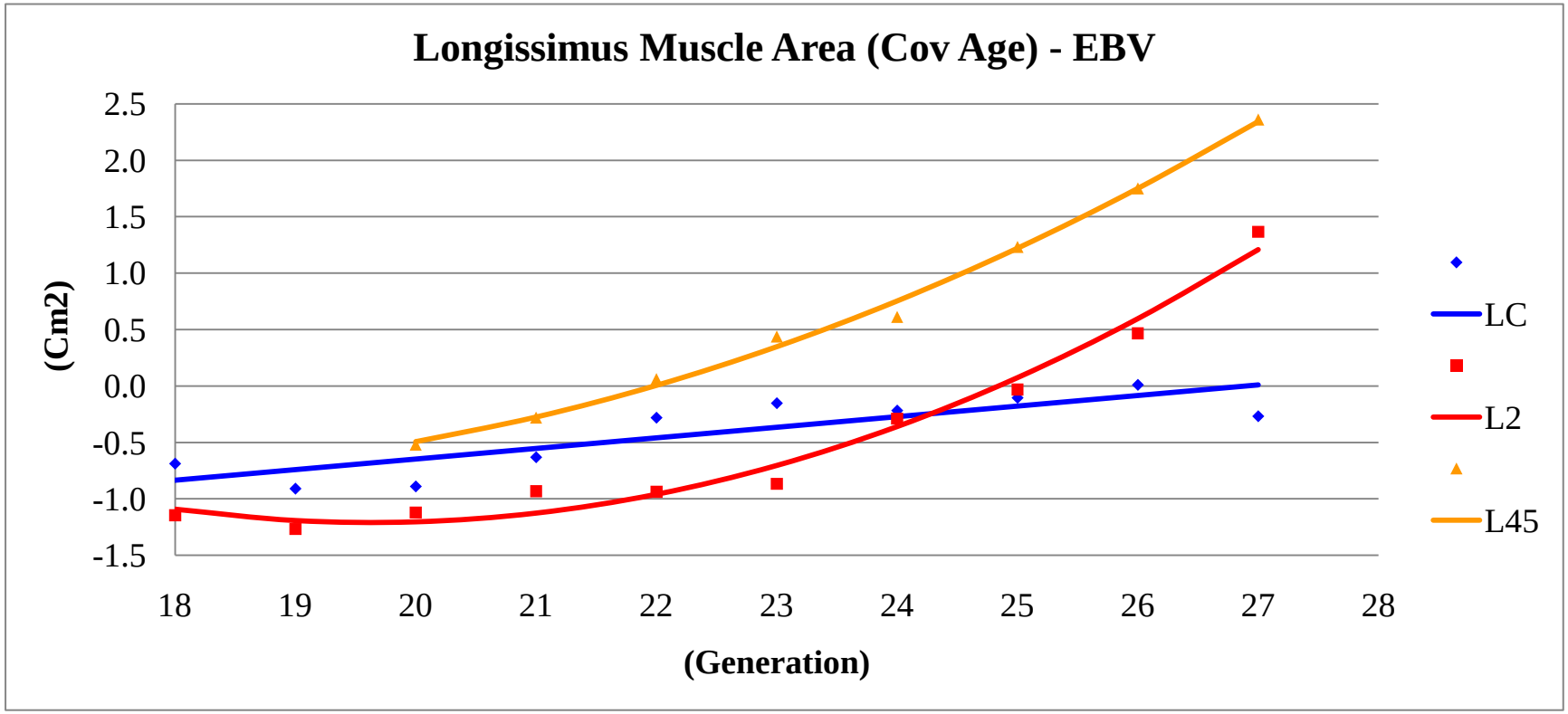

Figure 44. **Estimated genetic trends for longissimus muscle area with a covariate of age at age of final weight by line[a]**

[a] Lines:

LC was a control line in generation 18-28;

L2 was for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

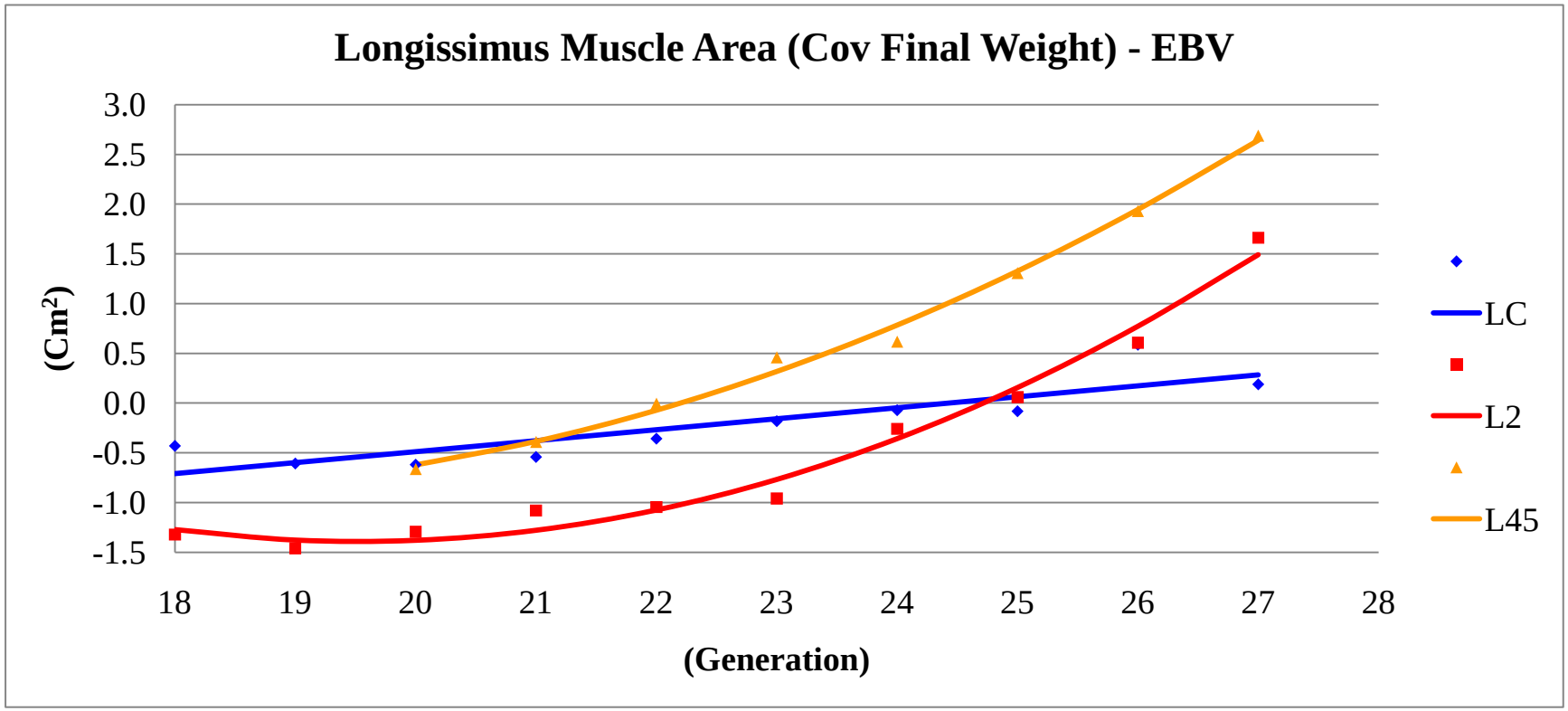

Figure 45. **Estimated genetic trends for longissimus muscle area with a covariate of final weight at age of final weight by line[a]**

[a] Lines:

LC was a control line in generation 18-28;

L2 was for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

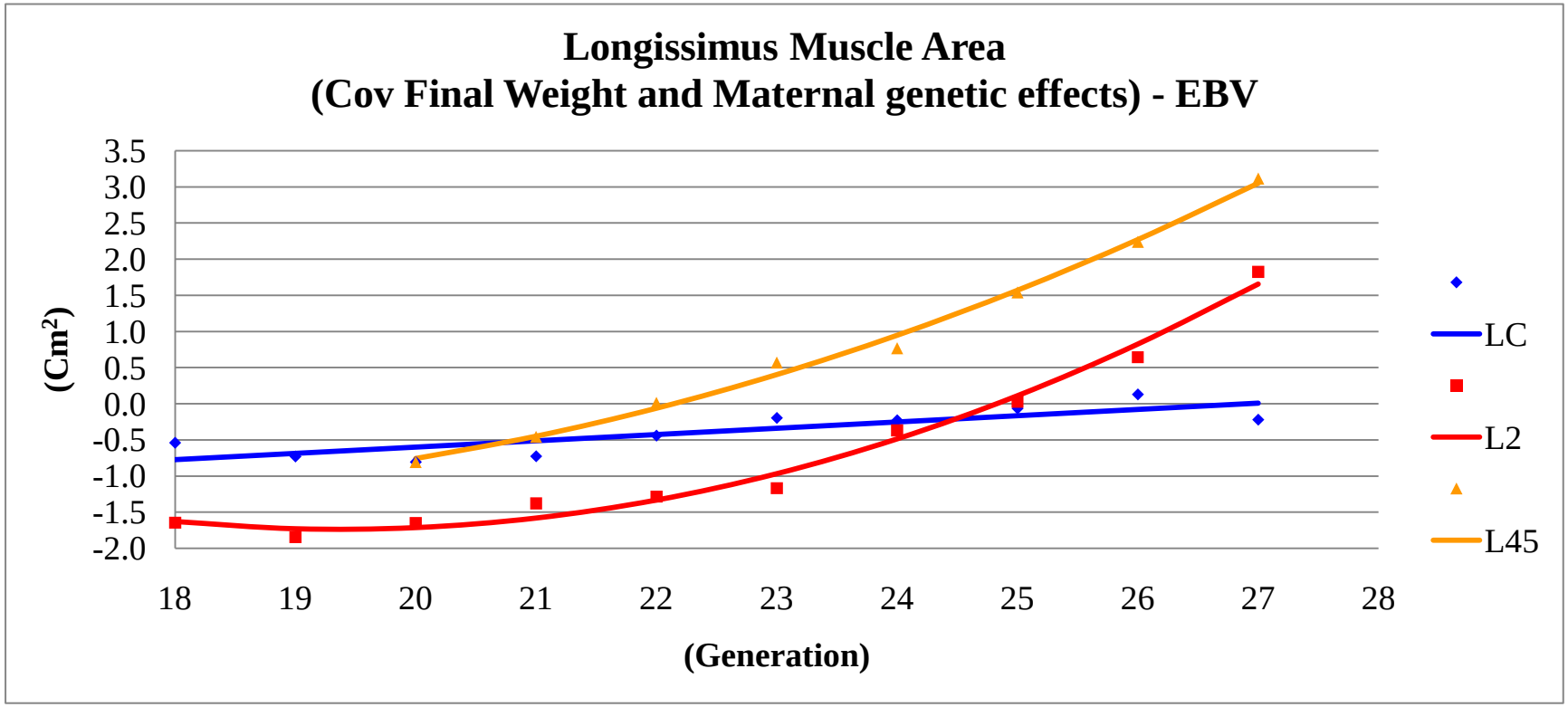

Figure 46. **Estimated genetic trends for longissimus muscle area with a covariate of final weight and random maternal genetic effects at age of final weight by line[a]**

[a] Lines:

LC was a control line in generation 18-28;

L2 was for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

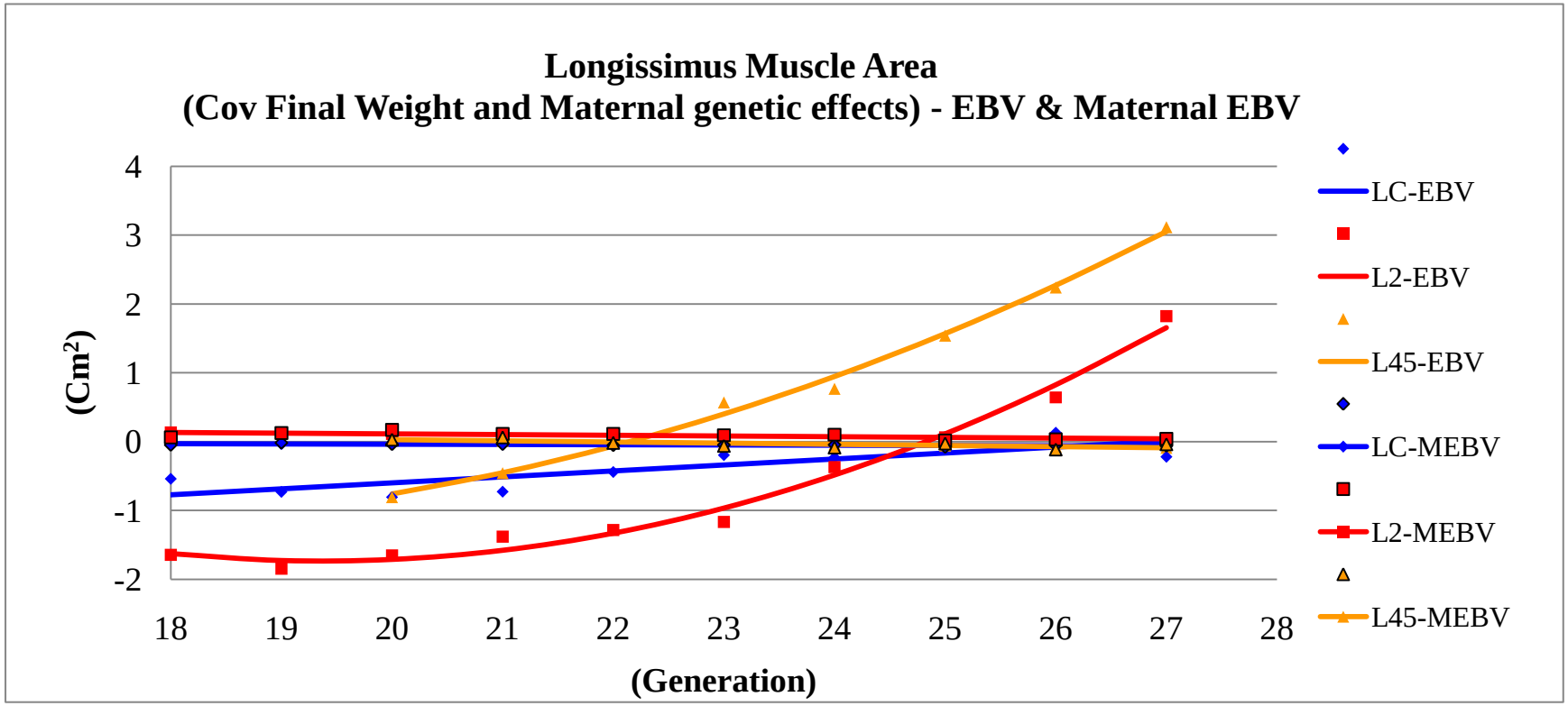

Figure 47. **Estimated direct and maternal genetic trends for longissimus muscle area with a covariate of final weight and random maternal genetic effects at age of final weight by line[a]**

a Lines:

LC was a control line in generation 18-28;

L2 was for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

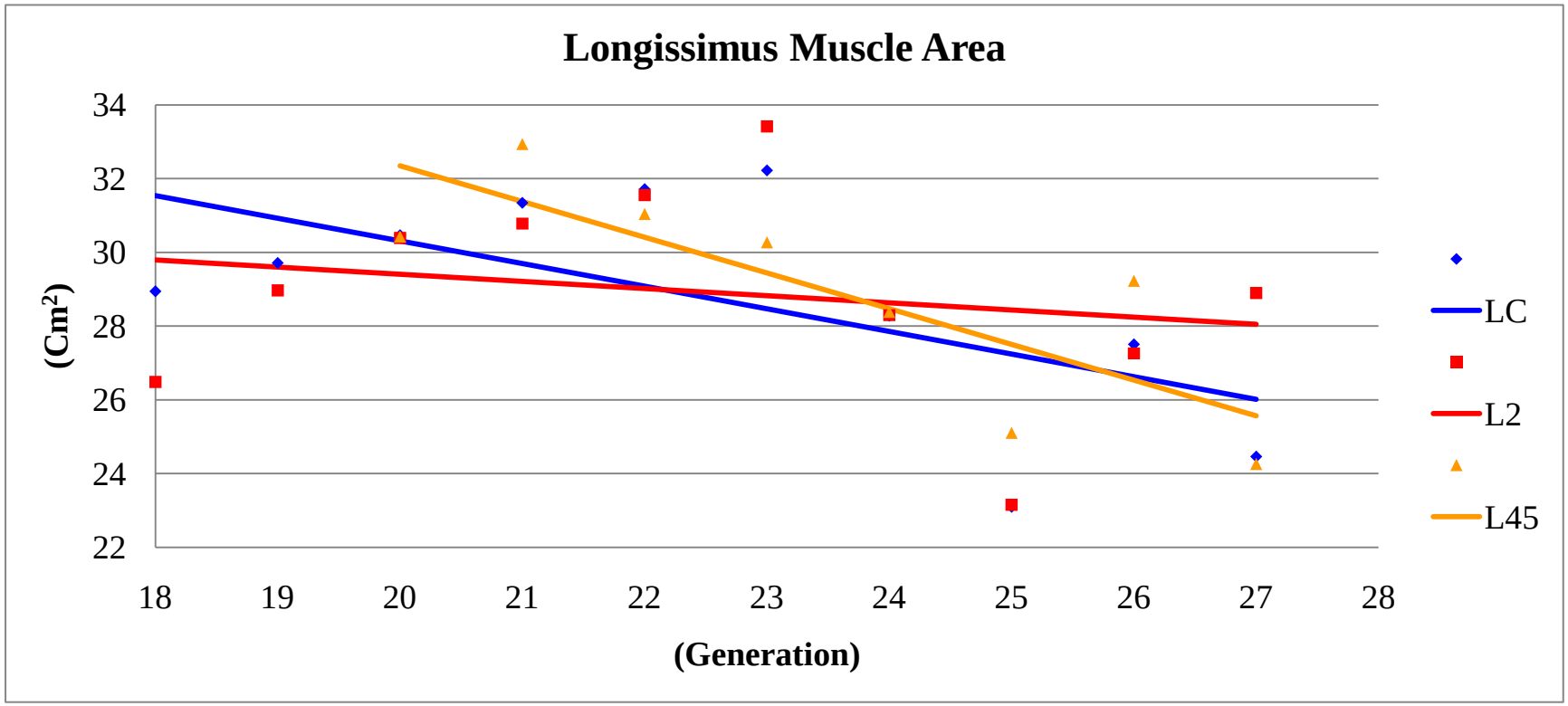

Figure 48. **Estimated phenotypic trends for longissimus muscle area with a covariate of age at age of final weight by line[a]**

[a] Lines:

LC was a control line in generation 18-28;

L2 was for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 20-28; L45 was selected for increased number of live pigs born per litter, increased growth rate, decreased backfat, and increased longissimus muscle area in generation 21-28.

Chapter 6

Literature Cited

Arango J., I. Misztal, S. Tsuruta, M. Culbertson, and W. Herring. 2005a. Threshold-linear estimation of genetic parameters for farrowing mortality, litter size, and test performance of Large White sows. J. Anim. Sci. 83:499-506.

Arango, J., I. Misztal, S. Tsuruta, M. Culbertson, and W. Herring. 2005b. Estimation of variance components including competitive effects of Large White growing gilts. J. Anim. Sci. 83:1241-1246.

Bakker H., J. H. Wallinga, and R. D. Politiek. 1978. Reproduction and body weight of mice after long-term selection for large litter size. J. Anim. Sci. 46:1572-1580.

Barria N., and G. E. Bradford. 1981a. Long-term selection for rapid gain in mice. I. Genetic analytical at the limit of response. J. Anim. Sci. 52:729-738.

Barria N., and G. E. Bradford. 1981b. Long-term selection for rapid gain in mice. II. Correlated changes in reproduction. J. Anim. Sci. 52:739-747.

Bennett G. L., and K. A. Leymaster. 1989. Integration of ovulation rate, potential embryonic viability and uterine capacity into a model of litter size in swine. J. Anim. Sci. 67:1230-1241.

Bennett G. L., and K. A. Leymaster. 1990a. Genetic implications of a simulation model of litter size in swine based on ovulation rate, potential embryonic

viability and uterine capacity: I. Genetic theroy. J. Anim. Sci. 68:969-979.

Bennett G. L., and K. A. Leymaster. 1990b. Genetic implications of a simulation model of litter size in swine based on ovulation rate, potential embryonic viability and uterine capacity: II. Simulated selection. J. Anim. Sci. 68:980-986.

Bergsma, R., Kanis, E., Knol, E. F. & Bijma, P. 2008. The contribution of social effects to heritable variation in finishing traits of domestic pigs (*Sus scrofa*). Genetics 178:1559–1570.

Bidanel J. P., J. Gruand, and C Legault. 1996. Genetic variability of age and weight at puberty, ovulation rate and embryo survival in gilts and relations with production traits. J. Anim. Sci. 28:103-115.

Blasco A., D. Sorensen, and J. P. Bidanel. 1998. Bayesian inference of genetic parameters and selection response for litter size components in pigs. Genetics. 149:301-306

Blasco A. J. A. Ortega, A. Climent, and M. A. Santacreu. 2005. Divergent selection for uterine capacity in rabbits. I. Genetic parameters and response to selection. J. Anim. Sci. 83:2297-2302.

Boldman, K. G., L. A. Kriese, L. D. Van Vleck, C. P. Van Tassell, and S. D. Kachman. 1995. A manual for use of MTDFREML. A set of programs to obtain estimates of variances and covariances [Draft]. USDA-ARS, Clay Center, NE.

Bolet G., L. Ollivier, and P. Dando. 1989. Selection for prolificacy in pigs. I Results

of a selection experiment over 11 generations. Genet., Sel.. Evol. 21:93-106.

Bradford G. E. 1979. Genetic variation in prenatal survival and litter size. J. Anim. Sci. 46(Suppl. 2):66-74.

Canario, L., N. Roy, J. Gruand, and J. P. Bidanel. 2006b. Genetic variation of farrowing kinetics traits and their relationships with litter size and perinatal mortality in French Large White sows. J. Anim. Sci. 84:1053–1058.

Cassady, J. P. & Van Vleck, L. D. 2004. Estimation of (co)variance components due to genetic competition effects in pigs. J. Anim. Sci. 82(Suppl.2):38. (Abstr.)

Chen P., T. J. Baas, J. W. Mabry, and K. J. Koehler. 2003. Genetic correlations between lean growth and litter traits in U.S. Yorkshire, Duroc, Hampshire, and Landrace pigs. J. Anim. Sci. 81:1700-1705.

Chen, C. Y., R. K. Johnson, S. D. Kachman, and L. D. Van Vleck. 2008. Estimation of genetic parameters for average daily gain using models with competition effects. J. Anim. Sci. 86:2525–2530.

Christenson R. K., K. A. Leymaster, and L. D. Young. 1987. Justification of unilateral hysterectomy-ovariectomy as a model to evaluate uterine capacity in swine. J. Anim. Sci. 65:738-744.

Cleveland E. R., R. K. Johnson, and P. J. Cunningham. 1988. Correlated respomses of carcass and reproductive traits to selection for rate of lean growth in swine. J. Anim. Sci. 66:1371-1377.

Cunningham P. J., M. E. England, L. D. Young and Dwane R. Zimmerman. 1979.

Selection for ovulation rate in swine: Correlation response in litter size and weight. J. Anim. Sci. 48:509-516.

Dziuk P. J. 1968. Effect of number of embryos and uterine space on embryo survival in the pig. J. Anim. Sci. 27:673-676.

Estany J., D. Villalba, J. Tibau, J. Soler, D. Babot, and J. L. Noguera. 2002. Correlated response to selection for litter size in pigs: I. Growth, fat deposition, and feeding behavior traits. J. Anim. Sci. 80:2556-2565.

Fredeen H. T., and H. Mikami. 1986a. Mass selection in a pig population: Experimental design and responses to direct selection for rapid growth and minimum fat. J. Anim. Sci. 62:1492-1508.

Fredeen H. T., and H. Mikami. 1986b. Mass selection in a pig population: Correlated responses in reproductive performance. J. Anim. Sci. 62:1523-1532.

Fredeen H. T., and H. Mikami. 1986c. Mass selection in a pig population: Correlated responses in preweaning growth. J. Anim. Sci. 62:1533-1545.

Fredeen H. T., and H. Mikami. 1986d. Mass selection in a pig population: Correlated changes in carcass merit. J. Anim. Sci. 62:1546-1554.

Haley, C. S., E. Avalos, and C. Smith. 1988. Selection for litter size in the pig. Anim. Breed. Abstr. 56:319-332.

Holl J. W., and O. W. Robison. 2003. Results from nine generations of selection for increased litter size in swine. J. Anim. Sci. 81:624-629.

Holm B., M. Bakken, G. Klemetsdal, and O. Vangen. 2004. Genetic correlations

between reproduction and production traits in swine. J. Anim. Sci. 82:3458-3464.

Hsu W. L., R. K. Johnson, and L. D. Van Vleck. 2010. Effect of pen mates on growth, backfat depth, and longissimus muscle area of swine. J. Anim. Sci. 88:895-902.

Jannink, J. L. 2003. Selection dynamics and limits under additive × additive epistatic gene action. Crop Sci. 43:489-497.

Johnson, R. K., D. R. Zimmerman, and R. J. Kittok. 1984. Selection for components of reproduction in swine. Livest. Prod. Sci. 11:541–558.

Johnson, R. K, M. K. Nielsen, and D. S. Casey. 1999. Responses in ovulation rate, embryo survival, and litter traits in swine to 14 generations of selection to increase litter size. J. Anim. Sci. 77:541-557.

Kerr, J. C., and N. D. Cameron. 1995. Reproductive performance of pigs selected for components of efficient lean growth. Anim. Sci. 60:281–290.

Lamberson, W. R., R. K. Johnson, D. R. Zimmerman, and T. E. Long. 1991. Direct responses to selection for increased litter size decreased age at puberty, or random selection following selection for ovulation rate in swine. J. Anim. Sci. 69:3129–3143.

Leenhouwers J. I., P. Wissink, T. van der Lende, H. Paridaans, and E. F. Knol. 2003. Stillbirth in the pig in relation to genetic merit for farrowing survival. J. Anim. Sci. 81:2419-2424.

Mesa H., T. J. Safranski, K. A. Fischer, K. M. Cammack, and W. R. Lamberson. 2005. Selection for placental efficiency in swine: Genetic parameters and trends. J. Anim. Sci. 83:983-991.

Neal S. M., R. K. Johnson, and R. J. Kittok. 1989. Index selection for components of litter size in swine: Response to five generations of selection. J. Anim. Sci. 67:1933-1945.

Noguera J. L., L. Varona, D. Babot, and J. Estany. 2002. Multivariate analysis of litter size for multiple parities with production traits in pigs: II. Response to selection for litter size and correlated response to production traits. J. Anim. Sci. 80:2548-2555.

Ollivier, L. 1982. Selection for prolificacy in the pig. Pig News Info. 3:383-388.

Roehe, R. 1999. Genetic determination of individual birth weight and its association with sow productivity traits using Bayesian analyses. J. Anim. Sci. 77:330-343.

Pérea-Enciso M, and J. P. Bidanel. 1997. Selection for litter size components: A critical review. J. Anim. Sci. 29:483-496.

Petry D. B., and R. K. Johnson. 2004. Responses to 19 generations of litter size selection in the Nebraska index line. I. Reproductive responses estimated in pure line and crossbred litters. J. Anim. Sci. 82:1000-1006.

Petry D. B., J. W. Holl, and R. K. Johnson. 2004. Responses to 19 generations of litter size selection in the NE index line. II. Growth and carcass responses estimated

in pure line and crossbred litters. J. Anim. Sci. 82:1895-1902.

Pope C. E., R. K. Christenson, V. A. Zimmerman-Pope, and B. N. Day. 1971. Effect of number of embryos on embryonic survival in recipient gilts. J. Anim. Sci. 35:805-808.

Rosendo A., T. Druet, J. Gogué, and J. P. Bidanel. 2007a. Direct responses to six generations of selection for ovulation rate or prenatal survival in Large White pigs. J. Anim. Sci. 85:356-364.

Rosendo A., T. Druet, J. Gogué, L. Canario, and J. P. Bidanel. 2007b. Correlated responses for litter traits to six generations of selection for ovulation rate or prenatal survival in French Large White pigs. J. Anim. Sci. 85:1615-1624.

Rosendo A., T. Druet, J. Gogué, L. Canario, and J. P. Bidanel. 2007c. Correlated responses of pre- and postweaning growth and backfat thickness to six generations of selection for ovulation rate or prenatal survival in French Large White pigs. J. Anim. Sci. 85:3209-3217.

Ruiz-Flores A., and R. K. Johnson. 2001. Direct and correlated responses to two-stage selection for ovulation rate and number of fully formed pigs at birth in swine. J. Anim. Sci. 79:2286-2297.

Santacreu M. A., M. L. Mocé, A. Climent, and A. Blasco. 2005. Divergent selection for uterine capacity in rabbits. II. Correlated response in litter size and its components estimated with a cryopreserved control population. J. Anim. Sci. 83:2303-2307.

SAS. 1996. SAS User's Guide (Release 6.09). SAS Inst. Inc., Cary, NC.

Schinckel, A. P., D. L. Lofgren, and M. E. Einstein. 1998. Resent stages index changes. Seedstock Edge, July Herdsire Issue: 120-121.

Sorensen, D., A. Vernersen, and S. Andersen. 2000. Bayesian analysis of response to selection: A case study using litter size in Danish Yorkshire pigs. Genetics 156:283–295.

Tess, M. W., G. L. Bennett, and G. E. Dickerson. 1983. Simulation of genetic changes in life cycle efficiency of pork production, H. Effects of components on efficiency. J. Anim. Sci. 56:354-368.

Tribout, T., J. C. Caritez, J. Gogué, J. Gruand, Y. Billon, M. Bouffaud, H. Lagant, J. Le Dividich, F. Thomas, H. Quesnel, R. Guéblez, and J. P. Bidanel. 2003. Estimation, par utilisation de semence congelée, du progrès génétique réalisé en France entre 1977 et 1998 dans la race porcine Large White: Résultats pour quelques caractères de reproduction femelle. Journées de la Recherche Porcine en France 35:285–292.

Webel S. K., and P. J. Dziuk. 1974. Effect of stage of gestation and uterine space on prenatal survival in the pigs. J. Anim. Sci. 38:960-963.

Wilson M. E., N. J. Biensen, and S. P. Ford. 1999. Novel insight into the control of litter size in pigs, using placental efficiency as a selection tool. J. Anim. Sci. 77:1654-1658.

Young L. D., R. J. Johnson, and I. T. Omtvedt. 1977. An analysis of the dependency

structure between a gilt's prebreeding and reproductive traits. I. Phenotypic and genetic correlations. J. Anim. Sci. 44:557-562.

Young L. D., R. A. Pumfrey, P. J. Cunningham, and Dwane R. Zimmerman. 1978. Heritabilities and genetic and phenotypic correlations for prebreeding traits, reproductive traits and principal components. J. Anim. Sci. 46:937-949.

Zimmerman Dwane R., and P. J. Cunningham. 1975. Selection for ovulation rate in swine: Population, procedures and ovulation response. J. Anim. Sci. 40:61-69.